

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2004, 09:51:51 ; Search time 45 Seconds
(without alignments)
1577.591 Million cell updates/sec

Title: US-10-006-922A-12
Perfect score: 1214
Sequence: 1 MRSSKNVKEFMRFKVRMEG.....EDYTIQEYERTEGRHHLFL 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1214	100.0	225	5	Q9U6Y8	Q9u6y8 discosoma s
2	1085.5	89.4	230	5	Q9GTU7	Q9gtj7 discosoma s
3	793	65.3	221	5	Q95P04	Q95p04 goniopora t
4	729.5	60.1	232	5	Q9U6Y7	Q9u6y7 discosoma s
5	690	56.8	225	5	Q963F5	Q963f5 montastraea s
6	681	56.1	225	5	Q95UA7	Q95ua7 montastraea s
7	681	56.1	225	5	Q7Z0W4	Q7z0w4 montastraea s
8	679.5	56.0	227	5	Q7Z0W6	Q7z0w6 montastraea s
9	678.5	55.9	227	5	Q962P9	Q962p9 montastraea s
10	678.5	55.9	227	5	Q7Z0W8	Q7z0w8 montastraea s
11	678	55.8	225	5	Q7Z0W5	Q7z0w5 montastraea s
12	669.5	55.1	234	5	Q7Z0W7	Q7z0w7 montastraea s
13	668.5	55.1	234	5	Q8T5F2	Q8t5f2 montastraea s
14	667	54.9	266	5	Q9U6Y3	Q9u6y3 clavularia
15	663	54.6	236	5	Q8T6U0	Q8t6u0 dendronephthya
16	655.5	54.0	227	5	Q95VT0	Q95vt0 montastraea s

17	654.5	53.9	234	5	Q8MU47	Q8mu47 montastraea s
18	652.5	53.7	225	5	Q7Z0W9	Q7z0w9 montastraea s
19	639	52.6	224	5	Q8MU48	Q8mu48 montastraea s
20	631.5	52.0	225	5	Q8T5F1	Q8t5f1 montastraea s
21	608.5	50.1	231	5	Q8ISF8	Q8isf8 parasicyoni
22	599.5	49.4	225	5	Q8IJU8	Q8ij8 trachyphyl
23	579.5	47.7	229	5	Q8MMA2	Q8mma2 agaricia fr
24	574	47.3	228	5	Q9GPI6	Q9gpi6 anemonia su
25	573.5	47.2	235	5	Q8T5F0	Q8t5f0 scolymia cu
26	570.5	47.0	231	5	Q8T6T8	Q8t6t8 discosoma s
27	566.5	46.7	239	5	Q8MMA1	Q8mma1 agaricia ag
28	559.5	46.1	231	5	Q8T5E9	Q8t5e9 ricordea fl
29	556.5	45.8	227	5	Q95W86	Q95w86 condylactis
30	556.5	45.8	232	5	Q9GPI5	Q9gpi5 anemonia su
31	556.5	45.8	232	5	Q9GZ28	Q9gz28 anemonia su
32	553.5	45.6	227	5	Q95W85	Q95w85 radianthus
33	551.5	45.4	231	5	Q8T5E8	Q8t5e8 ricordea fl
34	548.5	45.2	227	5	Q95W11	Q95w11 condylactis
35	546.5	45.0	231	5	Q8MU46	Q8mu46 ricordea fl
36	530.5	43.7	228	5	Q86LV4	Q86lv4 radianthus
37	530.5	43.7	234	5	Q8T5F3	Q8t5f3 scolymia cu
38	529.5	43.6	227	5	Q8MU45	Q8mu45 condylactis
39	522.5	43.0	225	5	Q8T6T9	Q8t6t9 radianthus
40	511.5	42.1	229	5	Q8T5E7	Q8t5e7 condylactis
41	495	40.8	229	5	Q9U6Y6	Q9u6y6 anemonia ma
42	490	40.4	214	5	Q86LV8	Q86lv8 meandrina m
43	490	40.4	214	5	Q86LV7	Q86lv7 meandrina m
44	485.5	40.0	231	5	Q9U6Y4	Q9u6y4 zoanthus sp
45	485.5	40.0	238	5	Q9BLV9	Q9blv9 renilla mue

ALIGNMENTS

RESULT 1

Q9U6Y8 PRELIMINARY; PRT; 225 AA.
ID Q9U6Y8
AC Q9U6Y8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Fluorescent protein FP583.
OS Discosoma sp.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;
OC Discosomatidae; Discosoma.
OX NCBI_TaxID=86600;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436614; PubMed=10504696;
RA Matz M.V., Fradkov A.F., Iabas Y.A., Savitsky A.P., Zaraisky A.G.,
RA Markelov M.L., Lukyanov S.A.;
RT "Fluorescent proteins from nonbioluminescent Anthozoa species.";
RL Nat. Biotechnol. 17:969-973(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Matz M.V., Fradkov A.F., Iabas Y.A., Savitsky A.P., Zaraisky A.G.,
RA Markelov M.L., Lukyanov S.A.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF168419; AAF03369.1; --
DR PDB; 1G7K; 07-NOV-01.
DR PDB; 1GGX; 06-DEC-00.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP_1.
DR PRINTS; PR01229; GFPUNRESCENT.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 225 AA; 25931 MW; FBF9A5369778F689 CRC64;

Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.4e-101;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query	1	MSRSKNV	IK	EFMR	FKVR	MEGT	VNG	HEFE	IEG	EGEG	RP	YEG	HN	TV	KL	KV	TK	GG	PL	P	F	A	M	D	I	60																															
Db	1	MSRSKNV	IK <td>EFMR<td>FKVR<td>MEGT<td>VNG<td>HEFE<td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	EFMR <td>FKVR<td>MEGT<td>VNG<td>HEFE<td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	FKVR <td>MEGT<td>VNG<td>HEFE<td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	MEGT <td>VNG<td>HEFE<td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	VNG <td>HEFE<td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	HEFE <td>IEG<td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	IEG <td>EGEG<td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	EGEG <td>RP<td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	RP <td>YEG<td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td></td>	YEG <td>HN<td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td></td>	HN <td>TV<td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td></td>	TV <td>KL<td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td></td>	KL <td>KV<td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td></td>	KV <td>TK<td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td></td>	TK <td>GG<td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td></td>	GG <td>PL<td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td></td>	PL <td>P<td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td></td>	P <td>F<td>A<td>M<td>D<td>I<td>60</td></td></td></td></td></td>	F <td>A<td>M<td>D<td>I<td>60</td></td></td></td></td>	A <td>M<td>D<td>I<td>60</td></td></td></td>	M <td>D<td>I<td>60</td></td></td>	D <td>I<td>60</td></td>	I <td>60</td>	60																															
QY	61	LSPOFOY	GSKV	YVKH	PA	DI	P	Y	K	L	S	P	E	G	F	K	M	E	R	V	M	N	F	E	D	G	V	T	Y	T	Q	D	S	L	Q	D	G	C	F	I	Y	120															
Db	61	LSPOFOY	GSKV	YVKH	PA	DI	P	Y	K	L	S	P	E	G	F	K	M	E	R	V	M	N	F	E	D	G	V	T	Y	T	Q	D	S	L	Q	D	G	C	F	I	Y	120															
QY	121	KV	K	F	I	G	V	N	F	P	S	D	G	P	V	M	Q	K	T	M	G	W	E	A	S	T	E	R	L	Y	P	R	D	G	V	L	K	G	E	I	H	K	A	L	K	D	G	H	Y	L	V	E	F	K	S	I	180
Db	121	KV	K	F	I	G	V	N	F	P	S	D	G	P	V	M	Q	K	T	M	G	W	E	A	S	T	E	R	L	Y	P	R	D	G	V	L	K	G	E	I	H	K	A	L	K	D	G	H	Y	L	V	E	F	K	S	I	180
QY	181	YMA	K	P	E	V	Q	L	P	G	Y	Y	V	D	S	K	L	D	I	T	S	H	N	E	D	Y	T	I	V	E	Q	Y	E	R	T	E	G	R	H	N	L	F	L	225													
Db	181	YMA	K	P	E	V	Q	L	P	G	Y	Y	V	D	S	K	L	D	I	T	S	H	N	E	D	Y	T	I	V	E	Q	Y	E	R	T	E	G	R	H	N	L	F	L	225													

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE GFP-like chromoprotein.
OS Goniopora tenuidens.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Fungiina; Poritidae; Goniopora.
OX NCBI_TaxID=75301;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21538626; PubMed=11682051;
RA Gurskaya N.G., Fradkov A.F., Tersikh A., Matz M.V., Labas Y.A.,
RA Martynov V.I., Yanushevich Y.G., Lukyanov K.A., Lukyanov S.A.;
RT "GFP-like chromoproteins as a source of far-red fluorescent
RT proteins(1).";
RL FEBS Lett. 507:16-20(2001).
EMBL: AF383156; AAL27542.1; -.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 221 AA; 24918 MW; 93F9F4B5C2003CB4 CRC64;

Query Match	65.3%	Score 793;	DB 5;	length 221;
Best Local Similarity	68.6%	Pred. No. 1.4e-63;		
Matches 144; Conservative	25;	Mismatches 41;	Indels 0;	Gaps 0;

[illegible]

RESULT 4			
ID	Q9U6Y7	PRELIMINARY;	PRT; 232 AA.
AC	Q9U6Y7;		
DT	01-MAY-2000 (TREMBUREl. 13, Created)		
DT	01-MAY-2000 (TREMBUREl. 13, Last sequence update)		
DT	01-OCT-2003 (TREMBUREl. 25, Last annotation update)		
DE	Fluorescent protein FP483.		
OS	Discosoma striata.		
OC	Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia;		
OC	Discosomatidae; Discosoma.		
OX	NCBI_TaxID=105400;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=99436614; PubMed=10504696;		
RA	Matz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zarskiy A.G.,		
RA	Markelov M.L., Lukyanov S.A.;		
RT	"Fluorescent proteins from nonbioluminescent Anthozoa species.";		
RL	Nat. Biotechnol. 17:969-973(1999).		
DR	EMBL: AF168420; AAF03370.1; -.		
DR	GO; GO:0006091; P:energy pathways; IEA.		
DR	InterPro; IPR009017; GFP_like.		
DR	InterPro; IPR000786; Green_fl_protein.		
DR	Pfam: PF01353; GFP.1.		
DR	PRINTS; PR01229; GFPUCRESCENT.		
DR	Prodom; PD013756; Green_fl_protein; 1.		
SO	SEQUENCE 232 AA; 26435 MW; AA8F18EEE283CE4D CR664;		

Query Match 60.1%; Score 729.5; DB 5; Length 232;
Best Local Similarity 59.1%; Pred. No. 8.2e-58;
Matches 133; Conservative 38; Mismatches 53; Indels 1; Gaps 1;
QY 1 MRSSKXVIEKMEFRKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAWDI 60
Db 1 MSCSKSVIKEMLIDLHLEGTFGNGHYFBIKKGKGQPNEGTNTVLTETKGGPLPFGWHI 60
QY 61 LSPQFYQGSKYVVKHPADIPDYKLSFPEGFKWRVMNPFEDGGVTVTTQDSSLQDGCIFY 120
Db 61 LCPQFYQGNKAFVHHPDNIHDYKLKSFPEGYTWERSMHFEDGGLCCITNDISLTGNCIFY 120
QY 121 KVKFIVNPPSDGVPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFESKI 180
Db 121 DIKFTGLNPPNGPVVQKTTGWEPSTERLYPRDGLIGDIHMLTVEGGGHYACDIKTV 180
QY 181 YMAKK-PVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHLF 224
Db 181 YRAKKAALKMPCGYHYVDTKLVIMNNDKEFMKVEHEIAVARHHPF 225

RESULT 5
Q963F5 PRELIMINARY; PRT; 225 AA.
ID Q963F5; AC Q963F5; DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Favina; Faviidae; Montastraea.
OX NCBI_TaxID=63558; RN [1]
RP SEQUENCE FROM N.A.
RA Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
RA Falkowski P., Gorbunov M., Kolber Z.;
RT "Green fluorescent proteins in Caribbean Scleractinian corals.";
RL Submitted (AUG-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF384683; AAK62982.2; -.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR00786; Green_fl_protein.
DR Pfam; PF01353; GFP. 1.
DR PRINTS; PR01229; GFPLORESCENT.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 225 AA; 25847 MW; 77DE7D7C616929AF CRC64;

Query Match 56.8%; Score 690; DB 5; Length 225;
Best Local Similarity 55.0%; Pred. No. 2.9e-54;
Matches 120; Conservative 44; Mismatches 54; Indels 0; Gaps 0;
QY 6 NVIKEMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAWDILSPQF 65
Db 2 SVIKPIMEIKLRMGGVNVNGHKFVIKGESEKPFEGTQTINLTVEKGAFLPFAYDILTSAF 61
QY 66 QYGSKYVVKHPADIPDYKLSFPEGFKWRVMNPFEDGGVTVTTQDSSLQDGCIFYKVKFI 125
Db 62 QYGNRVFTKYPDDIPDYFKQTFPEGYSWERIMAYEDQISCTATSDIKMEGDCFIYEIQFH 121
QY 126 GVNFPSSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFESKIYMAKK 185
Db 122 GVNFPNGPVVQKTKLKEPSTKMYVRDGLKGDVNMALLLEGGHYRCDFRSTYKAKK 181
QY 186 PVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGRHHL 223
Db 182 RVQLPDYHFVDHRIEILSHDNDYNTVKSSEDAEARYSM 219

RESULT 6
Q95UA7 PRELIMINARY; PRT; 225 AA.
ID Q95UA7; AC Q95UA7;

DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Cyân fluorescent protein (Fragment).
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Favina; Faviidae; Montastraea.
OX NCBI_TaxID=63558; RN [1]
RP SEQUENCE FROM N.A.
RA Falkowski P.G., Sun Y.;
RT "Montastraea cavernosa fluorescent protein."
RL Submitted (SEP-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY056460; AAL17905.1; -.
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR00786; Green_fl_protein.
DR Pfam; PF01353; GFP. 1.
DR PRINTS; PR01229; GFPLORESCENT.
DR ProDom; PD013756; Green_fl_protein; 1.
FT NON TER 225 225
SQ SEQUENCE 225 AA; 25775 MW; 52DE2F716D083524 CRC64;

Query Match 56.1%; Score 681; DB 5; Length 225;
Best Local Similarity 57.2%; Pred. No. 1.9e-53;
Matches 123; Conservative 36; Mismatches 56; Indels 0; Gaps 0;
QY 6 NVIKEMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAWDILSPQF 65
Db 2 SVIKSVMIKIKLRMDGIVNGHKFWITGESEKPFEGHTITILKVKEGGLPFAVDILTAF 61
QY 66 QYGSKYVVKHPADIPDYKLSFPEGFKWRVMNPFEDGGVTVTTQDSSLQDGCIFYKVKFI 125
Db 62 QYGNRVFTKYPKIDIPDYFKQSFPEGYSWERSMTFEDQVCTVTSIDIKLEGDCFFYEIRFY 121
QY 126 GVNFPSSDGPVMOCKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFESKIYMAKK 185
Db 122 GVNFPSSGPVMOCKTKLKEPSTENMYVRDGLLGDSRTLLLEGDKHRCNFRSTYGAKK 181
QY 186 PVQLPGYVYVDSKLDITSHNEDYTIIVEQYERTEGR 220
Db 182 GVLPEYHFVDHRIEILSHDKDYNTEVEYENAVAR 216

RESULT 7
Q7ZOW4 PRELIMINARY; PRT; 225 AA.
ID Q7ZOW4; AC Q7ZOW4; DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Chnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Favina; Faviidae; Montastraea.
OX NCBI_TaxID=63558; RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mc6;
RX MEDLINE=22689801; PubMed=12777529;
RA Kelmanson I.V., Matz M.V.;
RT "Molecular Basis and Evolutionary Origins of Color Diversity in Great
Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
RL Mol. Biol. Evol. 20:1125-1133(2003).
DR EMBL; AY181557; AAO61603.1; -.
SQ SEQUENCE 225 AA; 25827 MW; A600ADD716C5921E CRC64;

Query Match 56.1%; Score 681; DB 5; Length 225;
Best Local Similarity 54.6%; Pred. No. 1.9e-53;
Matches 119; Conservative 42; Mismatches 57; Indels 0; Gaps 0;
QY 6 NVIKEMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAWDILSPQF 65
Db 6 NVIKEMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAWDILSPQF 65

Db	2	SVLKPDMMKIKLRMEGAVNGHN	FVIEGEGKGP	PECTQTINL	TVKEGGPLP	FAYDIL	TLAA	61
QY	66	QYGSKYVVKHPADIPDYKKLSF	PPEGFKMERVNNFEDG	VTVTQDSSLQDGC	CFIYKVKFI	125		
Db	62	QYGNRAFTKYPRDIADYFKQSF	PPEGYSWERSMTYEDQICII	KSDIRMEGDC	CFIYEIRYD	121		
QY	126	GYNPSPDGPVMQOKKTMGWEAS	TERLYPRDGYLKG	IIHAKLKLKDG	GHYLV	EFKSI	YMAKK	185
Db	122	GYNFPSPGPMQOKKTLKMEPST	EKMYVRDGYLKG	DVNMALLLEG	GGHYRCDF	FRST	YKAKK	181
QY	186	PVQLBGIYVYVDSKLDITSHNE	DYTIIVEQYERTE	GRHHL	223			
Db	182	RYQLPDYHFVDHRIEILSHDND	YNTVKLS	EN	EARYSM	219		

```

RESULT 8
Q720W6
ID Q720W6 PRELIMINARY; PRT; 227 AA.
AC Q720W6;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mc4;
RX MEDLINE=22689801; PubMed=12777529;
RA Kelmanson I.V., Matz M.V.;
RT "Molecular Basis and Evolutionary Origins of Color Diversity in Great
RT Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
RL Mol. Biol. Evol. 20:1125-1133(2003).
DR EMBL; AY181555; AAO61601.1; -.
SQ SEQUENCE 227 AA; 26055 MW; 4BE2CB64FDB0E890 CRC64;

```

Query Match	56.0%;	Score 679.5;	DB 5;	Length 227;
Best Local Similarity	54.3%;	Pred. No. 2.6e-53;		
Matches 120;	Conservative 45;	Mismatches 53;	Indels 3;	Gaps 1;

[illegible]

```

RESULT 9
O962P9
ID O962P9 PRELIMINARY; PRT; 227 AA.
AC O962P9;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastrea faveolata.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Favina; Faviidae; Montastrea.
OX NCBI_TaxID=48498;
RN [1]
RP SEQUENCE FROM N.A.

```

RA Lesser M.P., Barry T.M., Mazel C., Matz M.V., Lukyanov S.A.,
 RA Falkowski P., Gorbunov M., Kolber Z.;
 RT "Green Fluorescent Proteins in Caribbean Scleractinian Corals.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401282; AAK83923.1; -.
 DR GO; GO:0006091; P:energy pathways; IEA.
 DR InterPro; IPR009017; GFP_like.
 DR InterPro; IPR000786; Green_fl_protein.
 DR Pfam; PF01353; GFP.1.
 DR ProDom; PD013756; Green_fl_protein; 1.
 SQ SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;

Query Match	55.94;	Score 678.5;	DB 5;	Length 227;
Best Local Similarity	54.8%;	Pred. No. 3.2e-53;		
Matches 121; Conservative	44;	Mismatches 53;	Indels 3;	Gaps 1;

```

QY      6 NVIKEFMRFKVRMEGTAVNGHEFELEBGEGERPYEGHNTVTKLVTKGGPLPEAMWILSPQF 65
      :||| : : :||| :||| : : :||| :||| : : :||| :||| : : :||| :||| :
Db      2 SVIKPDMKIKLRMEGAVNGHKFVIEGDGKGKPFEGTQSMDLTVKEGAPLPEFAYDILTVF 61

QY      66 QYGSKVYVKHPADIPDYKLSPPPEGFKMERVMNFEDGGVVTVTQDSSLQ--DGCFIYKV 122
      ||| : : :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db      62 DYGNRVFAKYPQDIPDYEFKQTEPEGYSWERSMTYEDQGIQVATINDITLMKGVDQCFVYKI 121

QY      123 KFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGLVKGELHKAALKLKDGHVLEFKSIYM 182
      :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db      122 RFDGVNFPA NGPVMQKKTLMKEBSTEKNYVRDGLVKGDVNMALLLEGGGHYRCDFTKTYK 181

QY      183 AKKPVQLPGYVVVDSKLDITSHNEDYTIIVEQYERTEGRHHH 223
      ||| ||| ||| :||| :||| :||| :||| :||| :||| :||| :||| :||| :
Db      182 AKKEVQLPDYHFDVDRHRIEILSHDKDYNKVKLYEHAEAHSGL 222

```

```

RESULT 10
Q7ZOW8
ID Q7ZOW8 PRELIMINARY; PRT; 227 AA.
AC Q7ZOW8;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Green fluorescent protein.
OS Montastraea cavernosa (great star coral).
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Scleractinia;
OC Faviina; Faviidae; Montastraea.
OX NCBI_TaxID=63558;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mc2;
RX MEDLINE=22689801; PubMed=12777529;
RA Kelmanson I.V., Matz M.V.;
RT "Molecular Basis and Evolutionary Origins of Color Diversity in Great
RT Star Coral Montastraea cavernosa (Scleractinia: Faviida).";
RL Mol. Biol. Evol. 20:1125-1133(2003).
DR EMBL; AY181553; AA061599.1; -.
SQ SEQUENCE 227 AA; 26017 MW; 5E312C54EA47F589 CRC64;

```

Query Match	55.9%;	Score 678.5;	DB 5;	Length 227;
Best Local Similarity	54.8%;	Pred. No. 3.2e-53;		
Matches 121; Conservative	44;	Mismatches 53;	Indels 3;	Gaps 1;

OY	6	NVIKEFMRFKVRMEGTVNGHEFEIEGEGBRPRYEGHNTVKLKVTYKGGLPFAMWILSPQF	65
Db	2	SVIKPDMKIKLRMGA VNGHKVIEGDGKGKPEEGTQSMDLTVEKGAFLPFA YDILTTFV	61
OY	66	QYGSKVYYKH PADIPDYKLSFPPEGFKMERVMNFEDGGVVTVTQBSLQ---DGCFIYKV	122
Db	62	DYGNRVFAKYPODIPDYKFQITPEEGYSWERSMTYEDOGICVATINDITLMKGVD DCFVYKI	121
OY	123	KFIGVNFPSSDGPWMÖKKTMGEASTERLYPRDGLTKGEIH KALKLKDGHYLVFEFSIYM	182
Db	122	RFDGVNFPANGPWÖKKTLKWPSTEKMYVRDGLKG DVNMALLLEGGGHYRCDFKTYYK	181
OY	183	AKKPVLPGYYYVDSKLDITSHNEDYTIVEÖYERTEGRHHL	223

DT 01-MAY-2000 (TReMBLrel. 13, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Fluorescent protein FP484.
OS Clavularia sp.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Alcyonacea;
OC Clavariidae; Clavularia.
OX NCBI_TaxID=86521;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99436614; PubMed=10504696;
RA Matcz M.V., Fradkov A.F., Labas Y.A., Savitsky A.P., Zaraisky A.G.,
RA Markelev M.L., Lukyanov S.A.;
RT "Fluorescent proteins from nonbioluminescent Anthozoa species.";
RL Nat. Biotechnol. 17:969-973(1999).
DR EMBL: AF168424; AAF03374.1; -
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PRO1229; GFLUORESCENT.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 266 AA; 30450 MW; B4E97406E2708854 CRC64;

Query Match 54.9%; Score 667; DB 5; Length 266;
Best Local Similarity 54.8%; Pred. No. 4.3e-52;
Matches 121; Conservative 42; Mismatches 58; Indels 0; Gaps 0;

QY 3 SSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDILS 62
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 41 TTMGVIKPDMKIKLKMEGNVNGHAFVIEGEGKPYDGTHTLTNLVKEGAPLPFSYDILS 100
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 63 PQFYGSKVYVKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFTYKV 122
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 101 NAFQYGNRALTKYPPDIADYFKQSFPEGYSWERTMTFEDKGIVKVKSDISMEDSFITYEI 160
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 123 KFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVFEKSIYM 182
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 161 RFDGMNFPNPGPVMQKTKLWEPSTEIMYVRDGLVGDISHSLLEGGGHYRCDFKSIYK 220
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 183 AKRPVOLPGYVVVDSKLDITSHNEDYTIIVEQYERTEGRHL 223
||| ||| : : ||| : : ||| : : ||| ||| : : |||
Db 221 AKKVVKLPDYHFVDHRIEILNHDKDYNKVTLYENAVARYSL 261
||| ||| : : ||| : : ||| : : ||| ||| : : |||

RESULT 15
Q8T6U0
ID Q8T6U0 PRELIMINARY; PRT; 236 AA.
AC Q8T6U0;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, last annotation update)
DE Green fluorescent protein.
OS Dendronephthya sp. SSAL-2002.
OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Alcyonaria; Alcyonacea;
OC Nephtheidae; Dendronephthya.
OX NCBI_TaxID=191210;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21927629; PubMed=11929996;
RA Labas Y.A., Gurskaya N.G., Yanushevich Y.G., Fradkov A.F.,
RA Lukyanov K.A., Lukyanov S.A., Matcz M.V.;
RT "Diversity and evolution of the green fluorescent protein family.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:4256-4261(2002).
DR EMBL: AF420591; AAM10625.1; -
DR GO; GO:0006091; P:energy pathways; IEA.
DR InterPro; IPR009017; GFP_like.
DR InterPro; IPR000786; Green_fl_protein.
DR Pfam; PF01353; GFP; 1.
DR PRINTS; PRO1229; GFLUORESCENT.
DR ProDom; PD013756; Green_fl_protein; 1.
SQ SEQUENCE 236 AA; 26840 MW; CE1707CFF9334A90 CRC64;

Query Match 54.6%; Score 663; DB 5; Length 236;

Best Local Similarity 55.6%; Pred. No. 8.4e-52;
Matches 120; Conservative 38; Mismatches 58; Indels 0; Gaps 0;
QY 6 NVIKFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDILSPQF 65
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 2 NLIKEDMRVKVMEGNVNGHAFVIEGEGKGRPYEGTQTLNLTVKEGAPLPFSYDILTAL 61
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 66 QYGSKYVYKHPADIPDYKKLSFPEGFKWERVMNFEDGGVVTVTQDSSLQDGCFTYKVF 125
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 62 HYGNRVFTLEYPADITDYFKQSFPEGYSWERTMTYEDKGICTIRSDISLEGDCFFQNTFRN 121
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 126 GVNFPDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVFEKSIYMAKK 185
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
Db 122 GGNFPNPGPVMQKTKLWEPSTEKLHVRDGLLVGNINMALLEGGGHYLCDFKTYAKK 161
: : ||| : : ||| ||| ||| ||| ||| ||| : : : : ||| : : |||
QY 186 PVQLPGYVVVDSKLDITSHNEDYTIIVEQYERTEGRH 221
||| ||| : : ||| : : ||| : : ||| ||| : : |||
Db 182 VVQLPDYHFVDHRIEILSNDSQYKVKLYEHGVARY 217
||| ||| : : ||| : : ||| : : ||| ||| : : |||

Search completed: July 8, 2004, 09:55:06
Job time : 47 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 8, 2004, 09:51:49 ; Search time 60 Seconds
(without alignments)
1059.553 Million cell updates/sec

US-10-006-922A-12

Perfect score: 1214
Sequence: 1 MRSSKNVIKEFMREFKVRMEG.....EDYTIIVEQYERTEGRHLLFL 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

```
Minimum DB seq length: 0
Maximum DB seq length: 20000000000
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

```
Database : A_Geneseq_29Jan04.*
1: geneseqp1980s.*
2: geneseqp1990s.*
3: geneseqp2000s.*
4: geneseqp2001s.*
5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	1214	100.0	225	3	AAY99836	Aay99836 Discosomana
2	1214	100.0	225	3	AAB01622	Aab01622 Discosomana
3	1214	100.0	225	4	AAG65509	Aag65509 Anthozoan
4	1214	100.0	225	5	ABB08834	Abb08834 Yeast optb
5	1214	100.0	225	5	AAE28833	Aae28833 Discosomana
6	1214	100.0	225	5	AAE17540	Aae17540 Discosomana
7	1214	100.0	225	5	AAO18270	Aao18270 Discosomana
8	1214	100.0	225	6	AAE34962	Aae34962 Discosomana
9	1214	100.0	225	7	ADC24126	Adc24126 Discosomana
10	1214	100.0	225	7	ABW00918	Abw00918 Discosomana
11	1214	100.0	487	5	ABB08821	Abb08821 Autofluor
12	1214	100.0	506	5	ABB08822	Abb08822 Autofluor
13	1214	100.0	547	5	ABB08823	Abb08823 Autofluor
14	1211	99.8	225	5	AAE28920	Aae28920 Discosomana
15	1211	99.8	225	7	ABW00937	Abw00937 Discosomana
16	1211	99.8	225	7	ABW00929	Abw00929 Discosomana
17	1211	99.8	225	7	ABW00938	Abw00938 Discosomana
18	1210	99.7	225	5	AAE28919	Aae28919 Discosomana
19	1210	99.7	225	7	ABW00930	Abw00930 Discosomana
20	1210	99.7	226	4	AAG65510	Aag65510 Anthozoan
21	1210	99.7	242	7	ADE24109	Ade24109 Discosomana
22	1209	99.6	225	5	AAE28922	Aae28922 Discosomana
23	1209	99.6	225	7	ABW00936	Abw00936 Discosomana
24	1209	99.6	225	7	ABW00931	Abw00931 Discosomana
25	1209	99.6	226	5	ABB08835	Abb08835 Yeast optb

26	1208	99.5	225	7	ABW00932	Abw00932	Discosoma
27	1208	99.5	225	7	ABW00935	Abw00935	Discosoma
28	1208	99.5	225	7	ABW00939	Abw00939	Discosoma
29	1207	99.4	225	5	AAE28921	Aae28921	Discosoma
30	1207	99.4	225	5	AAE17541	Aae17541	Discosoma
31	1207	99.4	225	7	ABW00941	Abw00941	Discosoma
32	1207	99.4	225	7	ABW00940	Abw00940	Discosoma
33	1206	99.3	225	7	ABW00933	Abw00933	Discosoma
34	1206	99.3	225	7	ABW00934	Abw00934	Discosoma
35	1205	99.3	240	6	ABP56678	Abp56678	Mammalian
36	1204	99.2	225	5	AAE28923	Aae28923	Discosoma
37	1204	99.2	225	5	AAE28925	Aae28925	Discosoma
38	1202	99.0	225	5	AAE28924	Aae28924	Discosoma
39	1202	99.0	240	6	ABP56685	Abp56685	Discosoma
40	1200	98.8	225	5	ABP70039	Abp70039	Colour Fa
41	1199	98.8	225	5	AAE28926	Aae28926	Discosoma
42	1199	98.8	240	6	ABP56684	Abp56684	Discosoma
43	1199	98.8	240	6	ABP56683	Abp56683	Discosoma
44	1194	98.4	240	6	ABP56681	Abp56681	Discosoma
45	1193	98.3	240	6	ABP56679	Abp56679	Discosoma

ALIGNMENTS

RESULT 1	
ID	AAAY99836 standard; protein; 225 AA.
AC	AAAY99836;
DT	12-SEP-2003 (revised)
DT	19-SEP-2000 (first entry)
DE	Discosoma sp. "red" novel fluorescent protein drFP583.
KW	Anthozoa; drFP583; fluorescent protein; non-bioluminescent organism; fluorescent labeling.
OS	Discosoma sp; "red".
FH	Key Location/Qualifiers
FT	Misc-difference 122
FT	/note= "encoded by TC"
FT	Misc-difference 127
FT	/note= "encoded by GTTG"
PN	WO200034326-A1.
PD	15-JUN-2000.
PF	10-DEC-1999; 99WO-US029473.
XX	
PR	11-DEC-1998; 98US-00210330.
PR	14-OCT-1999; 99US-00418529.
XX	
PA	(CLON-) CLONTECH LAB INC.
PI	Lukyanoy SA, Fradkov AF, Labas YA, Matz MV, Green G, Chen Y;
PI	Ding L;
XX	
DR	WPI; 2000-423381/36.
XX	
PT	Novel fluorescent protein from non-bioluminescent Discosoma sp. red,
PT	useful for fluorescent labeling and as markers.
XX	
PS	Claim 20; Page 74-75; 86pp; English.
XX	
CC	The present sequence is a novel fluorescent protein (nFP) encoded by the
CC	full-length cDNA drFP583. drFP583 was isolated from Discosoma sp. "red",
CC	a non-bioluminescent species of the class Anthozoa. Fluorescent proteins
CC	can be used in fluorescent labeling, a useful tool for marking a protein
CC	cell or organism of interest. Unlike other markers used in protein

XX The invention relates to nucleic acid molecules encoding non-aggregating
CC chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are
CC useful in analyte detection assays, as colouring agents, as markers in
CC recombinant DNA applications, as sunscreens or filters, in fluorescence
CC resonance energy transfer (FRET) applications, as biosensors in
CC prokaryotic and eukaryotic cells, in screening assays, as second
CC messenger detectors, in fluorescence activated cell sorting applications,
CC in protease cleavage assays or as fluorescent timers. The present
CC sequence is Discosoma sp. drFP583 (NFP-6) wild-type protein of the
XX invention
SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60

QY 61 LSPQFQYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
Db 61 LSPQFQYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120

QY 121 KVKFIGVNFPSDGPVMQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYLVFCKSI 180
Db 121 KVKFIGVNFPSDGPVMQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYLVFCKSI 180

QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 6
AAE17540
ID AAE17540 standard; protein; 225 AA.
XX
AC AAE17540;
XX
DT 22-APR-2002 (first entry)
XX
DE Discosoma sp. humanised wild-type Anthozoa protein drFP583.
XX
KW Fluorescent timer protein; protein movement; translocation; trafficking;
KW promoter activity; gene expression; transgenic plant; gene modification;
KW protein age; anthozoa protein; drFP583.
XX
OS Discosoma sp.
XX
PN WO200196373-A2.
XX
PD 20-DEC-2001.
XX
PF 13-JUN-2001; 2001WO-US019097.
XX
PR 14-JUN-2000; 2000US-0211607P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Fradkov AF, Tersikh A;
XX
DR WPI; 2002-154595/20.
DR N-PSDB; AAD28207.
XX
XX
PT New fluorescent timer proteins comprising an emission spectrum that
PT changes over time from a first wavelength to a second wavelength, useful
PT for monitoring intracellular protein movement, translocation, trafficking
PT or stability.
XX
PS Example 1; Fig 1; 89pp; English.
XX

CC The invention relates to a fluorescent timer protein having an emission
CC spectrum that changes over time after synthesis from a first wavelength
CC to a second wavelength. The fluorescent timer proteins are useful in
CC monitoring the activity of a promoter, determining the age of a protein,
CC identifying an agent that modulates the activity of a promoter and in
CC enriching a population of cells comprising a fluorescent timer protein.
CC The fluorescent timer proteins are also useful for assessing gene
CC expression during development of a multicellular organism or during
CC cellular differentiation, in response to a drug or other inducer of
CC promoter activity, as a reporter to serve as a read-out of promoter
CC activity, monitoring intracellular protein movement or translocation,
CC protein trafficking, or protein stability, to investigate temporal
CC aspects of the activity of a regulatory element, for determining cell
CC fate during development and organ remodelling, in spatial and temporal
CC visualisation of newly synthesised proteins and accumulated proteins, and
CC in distinguishing between newly formed and pre-existing structures, e.g.
CC membrane junctions and extracellular matrix components. The fluorescent
CC timer proteins may further be used to investigations where photobleaching
CC techniques are employed, as detectable labels, as selectable markers, as
CC biosensors in prokaryotic and eukaryotic cells, in protease cleavage
CC assays, and as second messenger detectors. The nucleic acids can be used
CC to generate transgenic, non-human plants or animals or site-specific gene
CC modifications in cell lines. The present sequence is Discosoma sp.
CC humanised wild-type Anthozoa protein drFP583 used for generating
XX fluorescent proteins
SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60

QY 61 LSPQFQYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
Db 61 LSPQFQYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120

QY 121 KVKFIGVNFPSDGPVMQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYLVFCKSI 180
Db 121 KVKFIGVNFPSDGPVMQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYLVFCKSI 180

QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 7
AAO18270
ID AAO18270 standard; protein; 225 AA.
XX
AC AAO18270;
XX
DT 26-SEP-2002 (first entry)
XX
DE Discosoma red fluorescent protein.
XX
KW Yeast; RAD54; promoter; genotoxicity cassette; cytotoxicity cassette;
KW modified yeast strain; environmental pollution.
XX
OS Discosoma sp.
XX
PN DE10061872-A1.
XX
PD 20-JUN-2002.
XX
PF 12-DEC-2000; 2000DE-01061872.
XX
PR 12-DEC-2000; 2000DE-01061872.
XX
PA (LICH/) LICHTENBERG-FRATE H.

XX Lichtenberg-Frate H;
PI
XX
DR WPI; 2002-539633/58.
DR N-PSDB; AAL47952.
XX
PT Modified yeast strain, useful for detecting toxic compounds in
PT environment, contains integrated cassettes responsive to genotoxic and
PT cytotoxic compounds.
XX
PS Disclosure; Page 21-22; 34pp; German.
XX
CC The present invention relates to a modified yeast strain that contains,
CC integrated stably and functionally in its genome, a genotoxicity cassette
CC and a cytotoxicity cassette, each comprising a promoter and reporter
CC gene, both of which are different in the two cassettes. The modified
CC yeast strain is used to detect environmental pollution, especially
CC genotoxic and/or cytotoxic substances in complex environmental
CC contaminants, especially organic compounds, but also (non-)ionising
CC radiation and chemical carcinogens. Particular applications are in
CC monitoring (waste) water (e.g. as an early warning system), medical
CC toxicology screening and for industrial process control. The present
CC sequence is a marker protein suitable for use in the cassettes of the
CC present invention
XX
SQ Sequence 225 AA;
SQ
Query Match 100.0%; Score 1214; DB 5; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAMWI 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAMWI 60
QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
DB 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
DB 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVVD SKLDTSHNEDYTYVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVVD SKLDTSHNEDYTYVEQYERTEGRHHLFL 225
RESULT 8
AAE34962
ID AAE34962 standard; protein; 225 AA.
XX
AC AAE34962;
XX
DT 28-MAY-2003 (first entry)
XX
DE Discosoma species red fluorescent protein (RFP).
XX
KW Phosphorylation indicator; fluorescent protein; detection; phosphatase;
KW kinase; red fluorescent protein; RFP.
XX
OS Discosoma sp.
XX
PN WO200295058-A2.
XX
PD 28-NOV-2002.
XX
PF 24-MAY-2002; 2002WO-US016955.
XX
PR 24-MAY-2001; 2001US-00865291.
XX
PA (REGC) UNIV CALIFORNIA.
XX

PI Tsien RY, Ting AY, Zhang J;
XX
DR WPI; 2003-148474/14.
DR N-PSDB; AAD53432.
XX
PT Novel chimeric phosphorylation indicators, useful for detecting
PT kinase/phosphatase in samples, has donor molecule, phosphorylatable
PT domain, phosphoaminoacid binding domain, and acceptor molecule, in
PT operative linkage.
XX
PS Disclosure; Col 65-66; 38pp; English.
XX
CC The present invention relates to chimeric phosphorylation indicators
CC comprising a phosphorylation polypeptide and a fluorescent protein or in
CC operative linkage, a donor molecule, a phosphorylatable domain, a
CC phosphoaminoacid binding domain (PABD) and an acceptor molecule. The
CC phosphorylation indicators of the invention are useful for detecting
CC kinases or phosphatases in a biological sample. They are also useful in
CC high throughput analysis e.g. for detecting a kinase inhibitor or
CC phosphatase inhibitor. The present sequence is Discosoma species red
CC fluorescent protein (RFP) used in the invention
XX
SQ Sequence 225 AA;
SQ
Query Match 100.0%; Score 1214; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAMWI 60
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAMWI 60
QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
DB 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVVTVTQDSSLQDGCFTY 120
QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
DB 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVVD SKLDTSHNEDYTYVEQYERTEGRHHLFL 225
DB 181 YMAKKPVQLPGYYVVD SKLDTSHNEDYTYVEQYERTEGRHHLFL 225
RESULT 9
ADC24126
ID ADC24126 standard; protein; 225 AA.
XX
AC ADC24126;
XX
DT 18-DEC-2003 (first entry)
XX
DE Discosoma wild-type red fluorescent protein.
XX
KW Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
KW fluorescent protein variant; transcription induction detection;
KW fluorescence energy resonance transfer; FRET; protein kinase;
KW protein phosphatase; ion indicator.
XX
OS Discosoma.
XX
PN US2003059835-A1.
XX
PD 27-MAR-2003.
XX
PF 10-APR-2002; 2002US-00121258.
XX
PR 26-FEB-2001; 2001US-00794308.
XX
PR 24-MAY-2001; 2001US-00866538.
XX
PA (TSIE/) TSIE R Y.
PA (CAMP/) CAMPBELL R E.
PA

XX Tsien RY, Campbell RE;
XX WPI; 2003-743764/70.
DR N-PSDB; ADC24127, ADC24134.
XX
PT Novel polynucleotide sequence encoding Discosoma red fluorescent protein
PT variant having a reduced propensity to oligomerize, useful for detecting
PT transcriptional activity.
XX
PS Claim 1; SEQ ID NO 1; 67pp; English.
XX
CC The invention describes a polynucleotide sequence (I) encoding a
CC Discosoma red fluorescent protein (DsRed) variant having a reduced
CC propensity to oligomerize, comprising amino acid substitutions at the AB
CC and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225
CC amino acids, given in the specification, where the substitutions result
CC in reduced propensity of the DsRed variant to form tetramers. (I) is
CC useful for detecting transcriptional activity by providing a host cells
CC containing a vector which comprises (I) operatively linked to an
CC expression control sequence, and an unit to assay the variant fluorescent
CC protein fluorescence, and assaying fluorescence of the variant
CC fluorescent protein produced by (VII), where variant fluorescent protein
CC fluorescence is indicative of transcriptional activity. A polynucleotide
CC encoding a fusion protein is useful for the analysis of in vivo
CC localization or trafficking of a polypeptide of interest. A polypeptide
CC marker is useful as markers to identify the location and amount of a
CC target protein produced, where the target protein is fused to the marker,
CC as a complement to or alternative for the green fluorescent protein or
CC its spectral variant, for detecting induction of transcripts, in
CC applications involving fluorescence energy resonance transfer (FRET),
CC which detects events as the function of the movement of fluorescent
CC donors and acceptors towards or away from each other, for making
CC fluorescent sensors for protein kinase and phosphatase activities or
CC indicators for ions and molecules such as Ca2+, Zn2+, for identifying the
CC presence of a molecule in a sample, for identifying a specific
CC interaction of a first and second molecule, for determining whether a
CC sample contains an enzyme or for determining the pH of the sample. (I) is
CC useful for identifying a region or condition that regulates the activity
CC of an expression control sequence. This is the amino acid sequence of
CC Discosoma wild-type red fluorescent protein.
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 1 MRSSKNVKEFMRFKVRMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60

QY 61 LSPQFGYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVTVTQDSSLQDGCFTY 120
Db 61 LSPQFGYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVTVTQDSSLQDGCFTY 120

QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGGHYLVEFKSI 180

QY 181 YMAKKPVQLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 10
ABW00918
ID ABW00918 standard; protein; 225 AA.
XX
AC ABW00918;
XX
DT 15-JAN-2004 (first entry)
XX

DE Discosoma sp. red fluorescent protein (RFP).
XX
XX Fluorescent protein; resonance energy transfer; pH; detection;
KM red fluorescent protein; RFP.
XX
XX Discosoma sp.
OS
XX US2003170911-A1.
PN
XX 11-SEP-2003.
PD
XX 26-FEB-2001; 2001US-00794308.
PF
XX 26-FEB-2001; 2001US-00794308.
PR
XX 26-FEB-2001; 2001US-00794308.
XX
PA (TSIE/) TSIE N Y.
PA (ZACH/) ZACHARIAS D A.
PA (BAIR/) BAIRD G S.
XX
PI Tsien RY, Zacharias DA, Baird GS;
XX
XX WPI; 2003-802418/75.
DR N-PSDB; AAD61969.
XX
PT Fluorescent proteins containing a mutation that reduces or eliminates its
PT ability to oligomerize which gives more reliable fluorescence resonance
PT energy transfer results and are useful to detect molecule interaction,
PT enzymes, or sample pH.
XX
PS Claim 10; Page 30-31; 0pp; English.
XX
CC The invention relates to a non-oligomerising fluorescent protein
CC containing a mutation that reduces or eliminates its ability to
CC oligomerize. The fluorescent protein gives more reliable fluorescence
CC resonance energy transfer results and are useful to detect molecule
CC interaction, enzymes, or sample pH. These are also used to identify
CC agents or conditions that regulate expression of control sequences. The
CC present sequence is Discosoma sp. red fluorescent protein (RFP)
XX
SQ Sequence 225 AA;

Query Match 100.0%; Score 1214; DB 7; Length 225;
Best Local Similarity 100.0%; Pred. No. 6.4e-128;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 1 MRSSKNVKEFMRFKVRMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60

QY 61 LSPQFGYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVTVTQDSSLQDGCFTY 120
Db 61 LSPQFGYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDGGVTVTQDSSLQDGCFTY 120

QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGGHYLVEFKSI 180

QY 181 YMAKKPVQLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYIYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225

RESULT 11
ABB08821
ID ABB08821 standard; protein; 487 AA.
XX
AC ABB08821;
XX
DT 28-MAY-2002 (first entry)
XX
DE Autofluorescent fusion protein A SEQ ID NO 1.
XX
KM Autofluorescent; fusion protein; proteolytic activity; fluorophore;

KW protease; assay; protease cleavage.
XX
OS Synthetic.
XX
PN WO200212543-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-EP009112.
XX
PR 07-AUG-2000; 2000DE-01038382.
XX
PA (DIRE-) DIREVO BIOTECH AG.
XX
PI Kuhlemann R, Koltermann A, Ketting U, Schwille P;
XX WPI; 2002-269094/31.
DR
XX
PT New autofluorescent fusion protein, useful for determining protease and
PT protease-inhibiting activity, comprises two different proteins linked by
PT protease cleavage site.
XX
PS Example; Page 11; 35pp; German.
XX
CC The invention relates to an autofluorescing fusion protein (I, ABB08821-
CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
CC segment containing a protease cleavage site; and (iii) at least one
CC different autofluorescing protein (Ib). Essentially no fluorescent energy
CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
CC quantifying protease (or protease-inhibitory) activity in liquid samples
CC or cells, particularly for screening-based optimisation (or generation)
CC of biomolecules with proteolytic activity. (I) can be prepared in
CC cellular or cell-free systems and makes possible intracellular analysis
CC of protease activity. Preparation of (I) does not require regioselective
CC coupling of fluorophores to polypeptides and any selected protease
CC cleavage site can be incorporated
XX
SQ Sequence 487 AA;

Query Match 100.0%; Score 1214; DB 5; Length 487;
Best Local Similarity 100.0%; Pred. No. 2e-127;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDI 60
Db 263 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDI 322
QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 120
Db 323 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 382
QY 121 KYKFIGVNFPSDGPVMQKKTWGEASTERLYPRDGLKGEIHKALKDKDGGHYLVEFKSI 180
Db 383 KYKFIGVNFPSDGPVMQKKTWGEASTERLYPRDGLKGEIHKALKDKDGGHYLVEFKSI 442
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 443 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 487

RESULT 12
ABB08822
ID ABB08822 standard; protein; 506 AA.
XX
AC ABB08822;
XX
DT 28-MAY-2002 (first entry)
XX
DE Autofluorescent fusion protein B SEQ ID NO 2.
XX
KW Autofluorescent; fusion protein; proteolytic activity; fluorophore;
KW protease; assay; protease cleavage.
XX

OS Synthetic.
XX
PN WO200212543-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-EP009112.
XX
PR 07-AUG-2000; 2000DE-01038382.
XX
PA (DIRE-) DIREVO BIOTECH AG.
XX
PI Kuhlemann R, Koltermann A, Ketting U, Schwille P;
XX WPI; 2002-269094/31.
DR
XX
PT New autofluorescent fusion protein, useful for determining protease and
PT protease-inhibiting activity, comprises two different proteins linked by
PT protease cleavage site.
XX
PS Claim 6; Page 11; 35pp; German.
XX
CC The invention relates to an autofluorescing fusion protein (I, ABB08821-
CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
CC segment containing a protease cleavage site; and (iii) at least one
CC different autofluorescing protein (Ib). Essentially no fluorescent energy
CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
CC quantifying protease (or protease-inhibitory) activity in liquid samples
CC or cells, particularly for screening-based optimisation (or generation)
CC of biomolecules with proteolytic activity. (I) can be prepared in
CC cellular or cell-free systems and makes possible intracellular analysis
CC of protease activity. Preparation of (I) does not require regioselective
CC coupling of fluorophores to polypeptides and any selected protease
CC cleavage site can be incorporated
XX
SQ Sequence 506 AA;

Query Match 100.0%; Score 1214; DB 5; Length 506;
Best Local Similarity 100.0%; Pred. No. 2.1e-127;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDI 60
Db 282 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTKGGLPFAWDI 341
QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 120
Db 342 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 401
QY 121 KYKFIGVNFPSDGPVMQKKTWGEASTERLYPRDGLKGEIHKALKDKDGGHYLVEFKSI 180
Db 402 KYKFIGVNFPSDGPVMQKKTWGEASTERLYPRDGLKGEIHKALKDKDGGHYLVEFKSI 461
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 225
Db 462 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHHLFL 506

RESULT 13
ABB08823
ID ABB08823 standard; protein; 547 AA.
XX
AC ABB08823;
XX
DT 28-MAY-2002 (first entry)
XX
DE Autofluorescent fusion protein C SEQ ID NO 3.
XX
KW Autofluorescent; fusion protein; proteolytic activity; fluorophore;
KW protease; assay; protease cleavage.
OS Synthetic.
XX

PN WO200212543-A2.
XX
PD 14-FEB-2002.
XX
PF 07-AUG-2001; 2001WO-EP009112.
XX
PR 07-AUG-2000; 2000DE-01038382.
XX
PA (DIRE-) DIREVO BIOTECH AG.
XX
PI Kuhlmann R, Koltermann A, Ketting U, Schwille P;
XX
DR WPI; 2002-269094/31.
XX
PT New autofluorescent fusion protein, useful for determining protease and
PT protease-inhibiting activity, comprises two different proteins linked by
PT protease cleavage site.
XX
PS Claim 6; Page 11; 35pp; German.
XX
CC The invention relates to an autofluorescing fusion protein (I, ABB08821-
CC ABB08823) comprising: (i) a first autofluorescing protein (Ia); (ii) a
CC segment containing a protease cleavage site; and (iii) at least one
CC different autofluorescing protein (Ib). Essentially no fluorescent energy
CC transfer occurs between (Ia) and (Ib). (I) is used for detecting and
CC quantifying protease (or protease-inhibitory) activity in liquid samples
CC or cells, particularly for screening-based optimisation (or generation)
CC of biomolecules with proteolytic activity. (I) can be prepared in
CC cellular or cell-free systems and makes possible intracellular analysis
CC of protease activity. Preparation of (I) does not require regioselective
CC coupling of fluorophores to polypeptides and any selected protease
CC cleavage site can be incorporated
XX
SQ Sequence 547 AA;

Query Match 100.0%; Score 1214; DB 5; Length 547;
Best Local Similarity 100.0%; Pred. No. 2.4e-127;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVIKEFMRFKVMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 323 MRSSKNVIKEFMRFKVMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 382

QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 120
Db 383 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 442

QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKGHYLVEFKSI 180
Db 443 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKGHYLVEFKSI 502

QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
Db 503 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 547

RESULT 14
AAE28920
ID AAE28920 standard; protein; 225 AA.
XX
AC AAE28920;
XX
DT 27-DEC-2002 (first entry)
XX
DE Discosoma sp. drFP583 (NFP-6) mutant protein, E5 (S197T).
XX
KW Fluorescent protein; chromoprotein; protease cleavage assay; filter;
KW fluorescence activated cell sorting application; fluorescent timer;
KW biosensor; fluorescence resonance energy transfer application; FRET;
KW colouring agent; recombinant DNA application; analyte detection assay;
KW sunsreen; second messenger detector; drFP583 protein; NFP-6; mutant;
mutain.
XX

OS Discosoma sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197 /note= "wild-type Ser substituted with Thr"
FT
XX
PN WO200268459-A2.
XX
PD 06-SEP-2002.
XX
PF 20-FEB-2002; 2002WO-US005749.
XX
PR 21-FEB-2001; 2001US-0270983P.
PR 04-DEC-2001; 2001US-00006922.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov S, Lukyanov K, Yanushkevich Y, Savitsky A, Fradkov A;
XX
DR WPI; 2002-691654/74.
XX
PT New nucleic acid encoding a non-aggregating chromo- or fluorescent mutant
PT of an aggregating Chidarian chromo- or fluorescent protein or mutant for
PT analyte detection assays or fluorescence activated cell sorting
PT applications.
XX
PS Disclosure; Page; 80pp; English.
XX
CC The invention relates to nucleic acid molecules encoding non-aggregating
CC chromo/fluorescent proteins and their mutants. Chromo/fluoro proteins are
CC useful in analyte detection assays, as colouring agents, as markers in
CC recombinant DNA applications, as sunscreens or filters, in fluorescence
CC resonance energy transfer (FRET) applications, as biosensors in
CC prokaryotic and eukaryotic cells, in screening assays, as second
CC messenger detectors, in fluorescence activated cell sorting applications,
CC in protease cleavage assays or as fluorescent timers. The present
CC sequence is Discosoma sp. drFP583 (NFP-6) mutant protein of the
CC invention. Note: This sequence is not shown in the specification, but is
CC derived from Discosoma sp. drFP583 (NFP-6) wild-type protein shown as SEQ
CC ID NO:8 (AAE28833) in page 70-71 of the specification
XX
SQ Sequence 225 AA;

Query Match 99.8%; Score 1211; DB 5; Length 225;
Best Local Similarity 99.6%; Pred. No. 1.4e-127;
Matches 224; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVIKEFMRFKVMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60
Db 1 MRSSKNVIKEFMRFKVMEGTVNGHFEIEGEGRPYEGHNTVKLKVTKGGLPFAMDI 60

QY 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 120
Db 61 LSPQFOYGSKVYVKHPADIPDYKKLSFPEGFKMERVMNFEDEGVTVTQDSSLQDGCFTY 120

QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKGHYLVEFKSI 180

QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
Db 181 YMAKKPVQLPGYVVYVDTKLDITSHNEDYTIIVEQYERTEGRHHFL 225

RESULT 15
ABW00937
ID ABW00937 standard; protein; 225 AA.
XX
AC ABW00937;
XX
DT 15-JAN-2004 (first entry)
XX

DE Discosoma sp. red fluorescent protein (RFP), S197T.
XX
KW Fluorescent protein; resonance energy transfer; pH; detection;
KW red fluorescent protein; RFP; mutant; mutein.
XX
OS Discosoma sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 197 /note= "Wild-type Ser is substituted with Thr"
XX
PN US2003170911-A1.
XX
PD 11-SEP-2003.
XX
PF 26-FEB-2001; 2001US-00794308.
XX
PR 26-FEB-2001; 2001US-00794308.
XX
PA (TSIE/) TSIE R Y.
PA (ZACH/) ZACHARIAS D A.
PA (BAIR/) BAIRD G S.
XX
PI Tsien RY, Zacharias DA, Baird GS;
XX
DR WPI; 2003-802418/75.
XX
PT Fluorescent proteins containing a mutation that reduces or eliminates its
PT ability to oligomerize which gives more reliable fluorescence resonance
PT energy transfer results and are useful to detect molecule interaction,
PT enzymes, or sample pH.
XX
PS Example 2; Page; 0pp; English.
XX
CC The invention relates to a non-oligomerising fluorescent protein
CC containing a mutation that reduces or eliminates its ability to
CC oligomerise. The fluorescent protein gives more reliable fluorescence
CC resonance energy transfer results and are useful to detect molecule
CC interaction, enzymes, or sample pH. These are also used to identify
CC agents or conditions that regulate expression of control sequences. The
CC present sequence is Discosoma sp. red fluorescent protein (RFP) mutant.
CC Note: This sequence is not shown in the specification, however this
CC sequence is constructed based on Discosoma sp. wild-type RFP protein
CC shown in page 30-31 (ABW00918)
XX
SQ Sequence 225 AA;

Query Match 99.8%; Score 1211; DB 7; Length 225;
Best Local Similarity 99.6%; Pred. No. 1.4e-127;
Matches 224; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVKLKVTKGGLPFAMD 60
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QY 121 KVKFICGVNFPSSDGPVMQKKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
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QY 181 YMAKKPVQLPGYYYVDSKLDITSHNEDYTIIVEQYERTEGRHHFL 225
Db 181 YMAKKPVQLPGYYYVDTKLDITSHNEDYTIIVEQYERTEGRHHFL 225

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 08:23:25 ; Search time 2083 Seconds
(without alignments)
14107.814 Million cell updates/sec

Title: US-10-006-922A-11

Perfect score: 678

Sequence: 1 atgaggtcttccaagaatgt.....gccaccatctgtcctttaa 678

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 2167151695 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
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17: em_hum:*
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27: em_sts:*
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30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
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39: em_htgo_hum:*
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41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	678	100.0	678	6 AR183915	AR183915 Sequence
2	678	100.0	678	6 AX172854	AX172854 Sequence
3	678	100.0	678	6 AX207715	AX207715 Sequence
4	678	100.0	678	6 AX233581	AX233581 Sequence
5	678	100.0	859	3 AF168419	AF168419 Discosoma
6	678	100.0	859	6 AX463698	AX463698 Sequence
7	665	98.1	666	6 AX348043	AX348043 Sequence
8	665	98.1	666	6 AX353910	AX353910 Sequence
9	658.8	97.2	898	6 AX686888	AX686888 Sequence
10	566.4	83.5	876	3 AF272711	AF272711 Discosoma
11	566.4	83.5	876	6 AX686894	AX686894 Sequence
12	449.8	66.3	681	6 AX233584	AX233584 Sequence
13	449.8	66.3	713	6 AX233627	AX233627 Sequence
14	449.2	66.3	678	6 AX370404	AX370404 Sequence
15	449.2	66.3	678	6 AX824725	AX824725 Sequence
16	447.2	66.0	4692	6 AX463702	AX463702 Sequence
17	447.2	66.0	9320	6 AX663075	AX663075 Sequence
18	446	65.8	678	6 AX370406	AX370406 Sequence
19	445.8	65.8	6893	6 AX823860	AX823860 Sequence
20	439.6	64.8	678	6 AX370408	AX370408 Sequence
21	438	64.6	678	6 AX824732	AX824732 Sequence
22	437	64.5	1050	6 AX666133	AX666133 Sequence
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28	410.2	60.5	1395	12 AF506026	AF506026 Synthetic
29	409.6	60.4	699	6 AR183914	AR183914 Sequence
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35	396	58.4	881	3 AF383156	AF383156 Goniorpora
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42	393.2	58.0	660	6 AX699817	AX699817 Sequence
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ALIGNMENTS

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LOCUS AR183915 678 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 6 from patent US 6342379.
ACCESSION AR183915
VERSION AR183915.1 GI:20227884
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 678)
AUTHORS Tsien,R.Y. and Gonzalez,J.E. III.
TITLE Detection of transmembrane potentials by optical methods
JOURNAL Patent: US 6342379-A 6 29-JAN-2002;
FEATURES Location/Qualifiers

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/organism="unknown"
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Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCTTCCAGAATGTTATCAAGAGGTTCAAGGTTTAAGGTTTCGATGGAAGA 60
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Db 1 ATGAGGTCTTCCAGAATGTTATCAAGAGGTTCAAGGTTTAAGGTTTCGATGGAAGA 60

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QY 661 CACCATCTGTCTCTTTAA 678
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Db 661 CACCATCTGTCTCTTTAA 678

RESULT 2
AX172854 678 bp DNA linear PAT 03-JUL-2001
LOCUS Sequence 6 from Patent WO0142211.
ACCESSION AX172854
VERSION AX172854.1 GI:14597903
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 T sien,R.Y. and Gonzalez,J.B.
AUTHORS Detection of transmembrane potentials by optical methods
TITLE Patent: WO 0142211-A 6 14-JUN-2001;
JOURNAL
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FEATURES The Regents of the University of California (US)
source location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 481 ATTCAATAGGCTCTGAAGCTGAAAGACGCGTGTGATCCTAGTTGAATTCAAAAGTATT 540
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Db 481 ATTCAATAGGCTCTGAAGCTGAAAGACGCGTGTGATCCTAGTTGAATTCAAAAGTATT 540

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QY 661 CACCATCTGTCTCTTTAA 678
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Db 661 CACCATCTGTCTCTTTAA 678

RESULT 3
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LOCUS Sequence 13 from Patent WO0157242.
ACCESSION AX207715
VERSION AX207715.1 GI:15422399
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
AUTHORS Corallimorpharia; Discosomatidae; Discosoma.
TITLE
JOURNAL
```

AUTHORS Stack,J.H., Whitney,M., Cubitt,A.B. and Pollok,B.A.
TITLE Methods of protein destabilization and uses thereof
JOURNAL Patent: WO 0157242-A 13 09-AUG-2001;
Aurora Biosciences Corporation (US)

FEATURES
source 1..678
/organism="Discosoma sp."
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ORIGIN

Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGAGGTCCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
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RESULT 4
LOCUS AX233581 678 bp DNA linear PAT 11-SEP-2001
DEFINITION Sequence 5 from Patent WO0162919.
ACCESSION AX233581
VERSION AX233581.1 GI:15593305
KEYWORDS
SOURCE Discosoma sp.
ORGANISM Discosoma sp.

REFERENCE
1 Nelson,D., Zamaira,E. and Tsien,R.
TITLE Modified fluorescent proteins
JOURNAL Patent: WO 0162919-A 5 30-AUG-2001;
Aurora Biosciences Corporation (US)

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Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 ATGAGGTCCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
Db 1 ATGAGGTCCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
Oy 61 ACGGTCAATGGGCACGAGTTTGAATAGAAGCGAAGAGAGAGAGAGAGAGAGAGAGAGAG 120
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Db 661 CACCATCTGTTCCCTTTAA 678

RESULT 5
LOCUS AF168419 859 bp mRNA linear INV 27-JUL-2001
DEFINITION Discosoma sp. fluorescent protein FP583 mRNA, complete cds.
ACCESSION AF168419

VERSION AF168419.2 GI:7105733
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
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REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
FEATURES

AF168419.2 GI:7105733
Discosoma sp.
Discosoma sp.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia; Discosomatidae; Discosoma.
1 (bases 1 to 859)
Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A.P., Zaraisky,A.G., Markelov,M.L. and Lukyanov,S.A.
Fluorescent proteins from nonbioluminescent Anthozoa species
Nat. Biotechnol. 17 (10), 969-973 (1999)
99436614
10504696
2 (bases 1 to 859)
Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A.P., Zaraisky,A.G., Markelov,M.L. and Lukyanov,S.A.
Direct Submission
Submitted (14-JUL-1999) Institute of Bioorganic Chemistry RAS, Miklukho-Maklaya 16/10, Moscow 117871, Russia
3 (bases 1 to 859)
Matz,M.V., Fradkov,A.F., Labas,Y.A., Savitsky,A.P., Zaraisky,A.G., Markelov,M.L. and Lukyanov,S.A.
Direct Submission
Submitted (25-FEB-2000) Institute of Bioorganic Chemistry RAS, Miklukho-Maklaya 16/10, Moscow 117871, Russia
Sequence update by submitter
On Feb 25, 2000 this sequence version replaced gi:6090866.
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CDS
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Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 234 TTGTCACCAATTTTCAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCCACATACCA 293
QY 241 GACTATAAAAGCTGTCAATTCCTGAAGATTTAATGGGAAAGGTCATGAACCTTGAA 300
DB 294 GACTATAAAAGCTGTCAATTCCTGAAGATTTAATGGGAAAGGTCATGAACCTTGAA 353
QY 301 GACGGTGGCGTCTTACTGTAAACCCAGGATTCAGTTTGACAGGATGGCTGTTTCATCTAC 360
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RESULT 6
AX463698
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

AX463698
Sequence 12 from Patent WO0248338.
AX463698
AX463698.1 GI:21886457
Discosoma sp.
Discosoma sp.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia; Discosomatidae; Discosoma.
1
Lichtenberg-Frat,H.
Yeast strain for testing the geno- and cytotoxicity of complex environmental contamination
Patent: WO 0248338-A 12 20-JUN-2002;
Lichtenberg-Frat, Heila (DE)
Location/Qualifiers
1..859
/organism="Discosoma sp."
/mol_type="unassigned DNA"
/db_xref="taxon:86600"
54..731
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD42147.1"
/db_xref="GI:21886458"
/db_xref="REMTREMBL:CAD42147"
/translation="MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTV
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GRHLFL"

CDS
ORIGIN

Query Match 100.0%; Score 678; DB 6; Length 859;
Best Local Similarity 100.0%; Pred. No. 7e-190;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAAAGATGTTATCAAGGAGTTCATGAGTTTAAAGTTCCGATGGAAGGA 60
DB 54 ATGAGGCTTCCAAAGATGTTATCAAGGAGTTCATGAGTTTAAAGTTCCGATGGAAGGA 113
QY 61 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGAAGAGAGGGGAGGCCATACGAAGGC 120
DB 114 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGAAGAGAGGGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTTGCCATTGCTTGGGATATT 180


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Db      174 CACAAATACCGTAAAGCTTAAAGTAAACCAAGGGGGACCTTGGCAATTGGCTTGGATATT 233
Oy      181 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCAACCTGCCGACATACCA 240
Db      234 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCAACCTGCCGACATACCA 293
Oy      241 GACTATAAAAGCTGTCAATTTCCGTAAGGATTTAATGGAAAGGTCATGAATTTGAA 300
Db      294 GACTATAAAAGCTGTCAATTTCCGTAAGGATTTAATGGAAAGGTCATGAATTTGAA 353
Oy      301 GACGGTGGCGTCTTACTGTAAACCCAGGATTTCCAGTTGCAAGATGGCTGTTTCACTAC 360
Db      354 GACGGTGGCGTCTTACTGTAAACCCAGGATTTCCAGTTGCAAGATGGCTGTTTCACTAC 413
Oy      361 AAGGTCAAAGTTCAATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAAGAGACA 420
Db      414 AAGGTCAAAGTTCAATTTGGCGTGAACCTTCTCCGATGACCTGTTATGCAAAAAGAGACA 473
Oy      421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTTGAAAGAGAG 480
Db      474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTTGAAAGAGAG 533
Oy      481 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAAGTATT 540
Db      534 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAAGTATT 593
Oy      541 TACATGGCAAGAAGCCCTGTGCAGCTACCAAGGTTACTACTATGTTGAATCCAAACTGGAT 600
Db      594 TACATGGCAAGAAGCCCTGTGCAGCTACCAAGGTTACTACTATGTTGAATCCAAACTGGAT 653
Oy      601 ATAACAAGCCACAACGAAGACTATATCAATCGTTGAGCAGATGAAAGAACCGAGGAGACGC 660
Db      654 ATAACAAGCCACAACGAAGACTATATCAATCGTTGAGCAGATGAAAGAACCGAGGAGACGC 713
Oy      661 CACCATCTGTCTCTTTAA 678
Db      714 CACCATCTGTCTCTTTAA 731

RESULT 7
AX348043      666 bp      DNA      linear      PAT 06-FEB-2002
LOCUS      AX348043
DEFINITION      Sequence 22 from Patent EP1172375.
ACCESSION      AX348043
VERSION      AX348043.1 GI:18614153
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Odenthal,M. and Jung,D.
TITLE      Gene expression, genome alteration and reporter gene expression in
              myofibroblasts and myofibroblasts-like cells by using the
              regulatory regions within the alpha smooth muscle alpha-actin gene
              Patent: EP 1172375-A 22 16-JAN-2002;
JOURNAL      Odenthal, Margarete (DE)
FEATURES
source      1..666
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Red Fluorescent Protein"
ORIGIN
Query Match      98.1%; Score 665; DB 6; Length 666;
Best Local Similarity      100.0%; Pred. No. 5e-186;
Matches 665; Conservative      0; Mismatches      0; Indels      0; Gaps      0;

Oy      13 AAGAATGTTATCAAGAGGTTTCATGAGTTTAAAGTTGCGATGGAAGAACGGTCAATGGG 72
Db      1 AAGAATGTTATCAAGAGGTTTCATGAGTTTAAAGTTGCGATGGAAGAACGGTCAATGGG 60
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Oy      73 CACGAGTTTGAATAGAAAGCGGAAGAGAGGGGAGGCCATACGAAGGCCACAATACCGTA 132
Db      61 CACGAGTTTGAATAGAAAGCGGAAGAGAGGGGAGGCCATACGAAGGCCACAATACCGTA 120
Oy      133 AAGCTTAAAGGTAACCAAGGGGGACCTTTGCCATTTGCTTTGGGATATTTTGTCAACACAA 192
Db      121 AAGCTTAAAGGTAACCAAGGGGGACCTTTGCCATTTGCTTTGGGATATTTTGTCAACACAA 180
Oy      193 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTTCCGACATACCAAGCTATATAAAG 252
Db      181 TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTTCCGACATACCAAGCTATATAAAG 240
Oy      253 CTGTCAATTTCTGGAAGGATTTAAATGGAAAGGGTCATGAACCTTGAAGACGGTGGCGTC 312
Db      241 CTGTCAATTTCTGGAAGGATTTAAATGGAAAGGGTCATGAACCTTGAAGACGGTGGCGTC 300
Oy      313 GTTACTGTAAACCCAGGATTTCCAGTTTGCAGATGGCTGTTTCACTACAAGGTCAAGTTC 372
Db      301 GTTACTGTAAACCCAGGATTTCCAGTTTGCAGATGGCTGTTTCACTACAAGGTCAAGTTC 360
Oy      373 ATGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAAGACAATGGCGTGGAA 432
Db      361 ATGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAAGACAATGGCGTGGAA 420
Oy      433 GCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTTGAAAGAGAGATTCATAAGGCT 492
Db      421 GCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTTGAAAGAGAGATTCATAAGGCT 480
Oy      493 CTGAAGCTGAAAGACGGTGTGATTAACCTAGTTGAATCAAAAAGTATTACATGGCAAAG 552
Db      481 CTGAAGCTGAAAGACGGTGTGATTAACCTAGTTGAATCAAAAAGTATTACATGGCAAAG 540
Oy      553 AAGCTGTGCAGCTACCAAGGTTACTATATGTTGACCTCCAACTGGATATACAAGCCAC 612
Db      541 AAGCTGTGCAGCTACCAAGGTTACTATATGTTGACCTCCAACTGGATATACAAGCCAC 600
Oy      613 AACGAAGACTATACAATCGTTGAGCAGATGAAAGAACCGAGGAGCCACCACATCTGTTTC 672
Db      601 AACGAAGACTATACAATCGTTGAGCAGATGAAAGAACCGAGGAGCCACCACATCTGTTTC 660

Oy      673 CTTTA 677
Db      661 CTTTA 665

RESULT 8
AX353910      666 bp      DNA      linear      PAT 06-FEB-2002
LOCUS      AX353910
DEFINITION      Sequence 22 from Patent WO0204509.
ACCESSION      AX353910
VERSION      AX353910.1 GI:18618888
KEYWORDS
SOURCE      .
ORGANISM      synthetic construct
              synthetic construct
              artificial sequences.
REFERENCE      1
AUTHORS      Odenthal,M. and Jung,D.
TITLE      Gene expression, genome alteration and reporter expression in
              myofibroblasts and myofibroblast-like cells
              Patent: WO 0204509-A 22 17-JAN-2002;
JOURNAL      Odenthal, Margarete (DE)
FEATURES
source      1..666
              /organism="synthetic construct"
              /mol_type="unassigned DNA"
              /db_xref="taxon:32630"
              /note="Red Fluorescent Protein"
ORIGIN
Query Match      98.1%; Score 665; DB 6; Length 666;
Best Local Similarity      100.0%; Pred. No. 5e-186;
Matches 665; Conservative      0; Mismatches      0; Indels      0; Gaps      0;
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QY	13	AAGAATGTTATCAAGGAGTTTCATGAGGTTTAAAGGTTCCGATGGAGAAAGCGGTCAATGGG	72
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QY	73	CACGAGTTTGAATAGAAAGCGAAGAGAGAGGGAGGCCATACGAAGGCCACAATACCCTA	132
Db	61	CACGAGTTTGAATAGAAAGCGAAGAGAGAGGGAGGCCATACGAAGGCCACAATACCCTA	120
QY	133	AAGCTTAAGGTAAACCAAGGGGGGACCTTGGCCATTGTGGGATATTTTGTCAACACAA	192
Db	121	AAGCTTAAGGTAAACCAAGGGGGGACCTTGGCCATTGTGGGATATTTTGTCAACACAA	180
QY	193	TTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACCAGACTATAAAAG	252
Db	181	TTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACCAGACTATAAAAG	240
QY	253	CTGTCAATTCCTGGAAGGATTTAAATGGGAAAAGGTCATGAATCTTGAAGACGGTGGCGTC	312
Db	241	CTGTCAATTCCTGGAAGGATTTAAATGGGAAAAGGTCATGAATCTTGAAGACGGTGGCGTC	300
QY	313	GTTACTGTAAACCCAGGATTCAGATTGCAAGATGGCTGTTCAATCTACAAGTCAAGTTC	372
Db	301	GTTACTGTAAACCCAGGATTCAGATTGCAAGATGGCTGTTCAATCTACAAGTCAAGTTC	360
QY	373	ATTGGCGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAAGABAACAATGGGCTGGAA	432
Db	361	ATTGGCGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAAGABAACAATGGGCTGGAA	420
QY	433	GCCAGCACTGAGCGTTTGATCTCTGTGATGCGCGTGTGAAAGAGAGATTCATAAGGCT	492
Db	421	GCCAGCACTGAGCGTTTGATCTCTGTGATGCGCGTGTGAAAGAGAGATTCATAAGGCT	480
QY	493	CTGAAGCTGAAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG	552
Db	481	CTGAAGCTGAAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG	540
QY	553	AAGCTGTGAGCTACCAGGGTACTACTATGTGTGACTCCAAACTGGATATAACAAGCCAC	612
Db	541	AAGCTGTGAGCTACCAGGGTACTACTATGTGTGACTCCAAACTGGATATAACAAGCCAC	600
QY	613	AACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGCCACCATCTGTTTC	672
Db	601	AACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGCCACCATCTGTTTC	660
QY	673	CTTTA 677	
Db	661	CTTTA 665	

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RESULT 9
AX686888
LOCUS      AX686888      898 bp      DNA      linear      PAT 31-MAR-2003
DEFINITION Sequence 11 from Patent WO0127150.
ACCESSION  AX686888
VERSION     AX686888.1   GI:29409468
KEYWORDS
SOURCE
ORGANISM   Discosoma sp.
            Discosoma sp.
            Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
            Corallimorpharia; Discosomacidae; Discosoma.
REFERENCE  1
AUTHORS    Lukyanov,S.A., Fradkov,A.F., Labas,Y.A., Matz,M.V. and Tersikh,A.
TITLE      Anthozoa derived chromo/fluoroproteins and methods for using the
            same
JOURNAL    Patent: WO 0127150-A 11 19-APR-2001;
            Clontech Laboratories Inc. (US)
FEATURES
            source
                location/Qualifiers
                1..898
                /organism="Discosoma sp."
                /mol_type="unassigned DNA"
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ORIGIN

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Query Match	97.2%	Score 658.8;	DB 6;	Length 898;
Best Local Similarity	98.2%	Pred. No. 3.5e-184;		
Matches 666; Conservative	0;	Mismatches 12;	Indels 0;	Gaps 0;

QY	1	ATGAGGTCCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGTTCCGATGGAAGGA	60
Db	93	ATGAGGTCCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGTTCCGATGGAAGGA	152
QY	61	ACGTCATATGGGCACGAGTTTGAATAAGAGCGGAAGGAGAGGGGACCATACGAAGGC	120
Db	153	ACGTCATATGGGCACGAGTTTGAATAAGAGCGGAAGGAGAGGGGACCATACGAAGGC	212
QY	121	CACAATACCGTAAAGCTTAAGTTAACCAAGGGGGGACCCTTGGCCAATTGCTTGGGATATT	180
Db	213	CACAATACCGTAAAGCTTAAGTTAACCAAGGGGGGACCCTTGGCCAATTGCTTGGGATATT	272
QY	181	TTGTCAACCACAATTTCAATATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA	240
Db	273	TTGTCAACCACAATTTCAATATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA	332
QY	241	GACTATATAAAAGCTGTCAATTCCTGAAGGATTTAATGGGAAGGTCATGAACTTTGA	300
Db	333	GACTATATAAAAGCTGTCAATTCCTGAAGGATTTAATGGGAAGGTCATGAACTTTGA	392
QY	301	GACGGTGGCGTCGTTACTGTAAACCAAGATTCCAGTTTGACAGATGGCTGTTTCATCTAC	360
Db	393	GACGGTGGCGTCGTTACTGTAAACCAAGATTCCAGTTTGACAGATGGCTGTTTCATCTAC	452
QY	361	AAGGTCAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGGAAGACA	420
Db	453	AAGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGGAAGACA	512
QY	421	ATGGGCTGGGAAGCCAGCACTGAGCCGTTTGATCTCTCGTATGGCGTGTGAAAGGAGAG	480
Db	513	ATGGGCTGGGAAGCCAGCACTGAGCCGTTTGATCTCTCGTATGGCGTGTGAAAGGAGAG	572
QY	481	ATTCAATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT	540
Db	573	ATTCAATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT	632
QY	541	TACATGGCAAGAAGCCTGTGCACTACCAAGGTACTACTATGTTGACTCCAAACTGGAT	600
Db	633	TACATGGCAAGAAGCCTGTGCACTACCAAGGTACTACTATGTTGACTCCAAACTGGAT	692
QY	601	ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACGAGGAGCGC	660
Db	693	ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACGAGGAGCGC	752
QY	661	CACCATCTGTTCTTTAA 678	
Db	753	CACCATCTGTTCTTTAA 770	

RESULT	10
LOCUS	AF272711
DEFINITION	AF272711 876 bp mRNA linear INV 26-SEP-2000 Discosoma sp. SSAL-2000 red fluorescent protein (FP593) mRNA, complete cds.
ACCESSION	AF272711
VERSION	AF272711.1 GI:10304306
KEYWORDS	.
SOURCE	Discosoma sp. SSAL-2000
ORGANISM	Discosoma sp. SSAL-2000 Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Corallimorpharia; Discosomatidae; Discosoma. 1 (bases 1 to 876)
REFERENCE	Fradkov,A.F., Chen,Y., Ding,L., Barsova,E.V., Matz,M.V. and AUTHORS Lukyanov,S.A.
TITLE	Novel fluorescent protein from Discosoma coral and its mutants possesses a unique far-red fluorescence
JOURNAL	FEBS Lett. 479 (3), 127-130 (2000)
MEDLINE	20434599
PUBMED	10981720

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REFERENCE          2 (bases 1 to 876)
AUTHORS            Fradkov,A.F., Chen,Y., Ding,L., Barsova,E.V., Maltz,M.V. and
                    Lukyanov,S.A.
TITLE              Direct Submission
JOURNAL            Submitted (26-MAY-2000) Institute of Bioorganic Chemistry RAS,
                    Miklukho-Maklaya 16/10, Moscow 117871, Russia
FEATURES
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  gene              1. 876
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                    /note="d8FP593"
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                    /db_xref="GI:10304307"
                    /translation="MSCSKNVYKEFMRFKVRMEGTVNGHEPEIKGEGERPYEGHCSV
                    KLVTKGGPLPEAFDILSPFOGSKVYVKHPADIPDYKXLSPEGFKEKRVNMFEDG
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ORIGIN
Query Match       83.5%; Score 566.4; DB 3; Length 876;
Best Local Similarity 90.6%; Pred. No. 9.5e-157;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
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Db               645 GATATGACGAGCCACAAAGAAATTACACAGTCGTTGAGCAGTATGAAAAAACCCAGGA 704
Qy               658 CGCCACCATCTGTTCTTTA 677
Db               705 CGCCACCATCCGTTCAATTAA 724

RESULT 11
AX686894          876 bp      DNA      linear      PAT 31-MAR-2003
LOCUS             AX686894
DEFINITION        Sequence 17 from Patent WO0127150.
ACCESSION         AX686894
VERSION           AX686894.1 GI:29409472
KEYWORDS
SOURCE
ORGANISM          Discosoma sp.
                  Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia;
                  Corallimorpharia; Discosomatidae; Discosoma.

REFERENCE          1
AUTHORS            Lukyanov,S.A., Fradkov,A.F., Labas,Y.A., Maltz,M.V. and Tersikh,A.
TITLE              Anthozoa derived chromo/fluoroproteins and methods for using the
                    same
JOURNAL            Patent: WO 0127150-A 17 19-APR-2001;
                    Clontech Laboratories Inc. (US)
FEATURES
  source            1. 876
                    /organism="Discosoma sp."
                    /mol_type="unassigned DNA"
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ORIGIN
Query Match       83.5%; Score 566.4; DB 6; Length 876;
Best Local Similarity 90.6%; Pred. No. 9.5e-157;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
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Db	585	TACATGTTAAGAAGCCTTCAGTGCAGTTGCCAGGCTACTATATGTGACTCCAAC	644
QY	598	GATATAACAAGCCCAACAAGAGACTATACAATCGTTGAGCAGTATGAAGAACCGAGGGA	657
Db	645	GATATGACGAGCCACAACAAGATTACACAGTCGTTGAGCAGTATGAAGAAACCAGAGGA	704
QY	658	CGCCACCATCTGTTCTTTA	677
Db	705	CGCCACCATCCGTTCAATTAA	724
RESULT 12			
AX233584		681 bp	DNA
LOCUS	AX233584		linear
DEFINITION	Sequence 8 from Patent WO0162919.		PAT 11-SEP-2001
ACCESSION	AX233584		
VERSION	AX233584.1	GI:15593307	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1		
AUTHORS	Nelson,D., Zamaira,E. and Tsien,R.		
TITLE	Modified fluorescent proteins		
JOURNAL	Patent: WO 0162919-A 8 30-AUG-2001;		
	Aurora Biosciences Corporation (US)		
FEATURES			
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CDS	1..681		
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	EGRHHLFL"		
ORIGIN			
Query Match	66.3%;	Score 449.8;	DB 6; Length 681;
Best Local Similarity	79.0%;	Pred. No. 3.9e-122;	
Matches	535;	Conservative 0;	Mismatches 142; Indels 0; Gaps 0;
QY	2	TGAGGTCTTCCAAGAATGTTATCAAGAGTTCATGAGTTTAAGTTCCGATGGAAGAA	61
Db	5	TGAGGAGCAGCAAGAACGTGATCAAGAGTTCATGAGTTCAAGGTGCGCATGAGGGCA	64
QY	62	CGGTCAATGGGCACGAGTTGAAATAGAAAGCGAAAGGAGAGGGGCGCATACGAAGCC	121
Db	65	CCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCTACGAGGGCC	124
QY	122	ACAATACCGTAAGCTTAAGTAAACCAAGGGGGGACCTTTGCCATTGCTTGGAATTT	181
Db	125	ACAACAACCGTGAAGCTTAAGGTGACCAAGGGGGGGCCCTGCTTCCCTGGGACATCC	184
QY	182	TGTCAACCACAATTCAGTATGGAAGCAAGGTATATGTCACACCCCTGCCGACATACCAG	241
Db	185	TGAGCCCCCAGTTCAGTACGGCAGCAAGGTGTACGTGAAGCAACCCCGGACATCCCG	244
QY	242	ACTATAAAAAGCTGTCAATTCCTGAAGGATTTAAATGGGAAAAGGTCATGAATTTGAAG	301
Db	245	ACTACAAGAAGCTGAGCTTCCCGAGGGCTTCAAGTGGAAGAGGGTGATGAATTCGAGG	304
QY	302	ACGGTGGCGTCTTACTGTAAACCGAGATTCAGTTTGACAGATGGCTGTTCACTTACA	361
Db	305	ACGGCGGCGTGTGACCGTGACCAAGACAGACAGCCTGCAAGACGGCTGCTTCACTTACA	364

QY	362	AGGTCAAGTTCAATTGGCGTGAACCTTTCCTCCGATGAGACCTGTTATGCAAAAAGAGACA	421
Db	365	AGGTGAAGTTCAATCGCGCGTGAACCTTCCCGAGCAGCGCCCCCGTGAATGCAAGAAAGACCA	424
QY	422	TGGCTGGGAAGCCAGCACTGAGCGTTGTATCTCTCGTATGGCGTGTGAAAGGAGAGA	481
Db	425	TGGCTGGGAGGCTCCACCGAGCGCTGTACCCCCCGCAGCGCGGTGTGAAGGGCGAGA	484
QY	482	TTCATAAGGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATTT	541
Db	485	TCCACAAGGCCCTGAAGCTGAAGAGCGGCGCCACTACCTGTGTGAGTTCAAGTCCATCT	544
QY	542	ACATGGCAAGAAGCCTGTGCAAGCTACAGGGTACTACTATGTGACTCCAAACTGATTA	601
Db	545	ACATGGCCAGAAGCCCGTGCAAGCTGCCCGCTACTACTAGTGGACTCCAAAGCTGACA	604
QY	602	TACACAGCCCAACGAAGACTATACATCGTTGAGCAGCATATGAAGAACCGAGGACGCC	661
Db	605	TCACCAAGCCCAACGAAGACTACACCATCTGTGAGCAGTACGAGAGGACCGAGGCGAGGC	664
QY	662	ACCATCTGTTCTTTAA	678
Db	665	ACCACCTGTTCTGTGA	681

RESULT 13			
AX233627		713 bp	DNA
LOCUS	AX233627		linear
DEFINITION	Sequence 51 from Patent WO0162919.		PAT 11-SEP-2001
ACCESSION	AX233627		
VERSION	AX233627.1	GI:15593330	
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE	1		
AUTHORS	Nelson,D., Zamaira,E. and Tsien,R.		
TITLE	Modified fluorescent proteins		
JOURNAL	Patent: WO 0162919-A 51 30-AUG-2001;		
	Aurora Biosciences Corporation (US)		
FEATURES			
source	1..713		
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ORIGIN			
Query Match	66.3%;	Score 449.8;	DB 6; Length 713;
Best Local Similarity	79.0%;	Pred. No. 3.9e-122;	
Matches	535;	Conservative 0;	Mismatches 142; Indels 0; Gaps 0;
QY	2	TGAGGTCTTCCAAGAATGTTATCAAGAGTTCATGAGTTTAAGTTCCGATGGAAGAA	61
Db	23	TGAGGAGCAGCAAGAACGTGATCAAGAGTTCATGAGTTCAAGGTGCGCATGAGGGCA	82
QY	62	CGGTCAATGGGCACGAGTTGAAATAGAAAGCGAAAGGAGAGGGGCGCATACGAAGGCC	121
Db	83	CCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCCTTACGAGGGCC	142
QY	122	ACAATACCGTAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTGCTTGGAATTT	181
Db	143	ACAACAACCGTGAAGCTTAAGGTGACCAAGGGGGGGCCCTGCTTCCCTGGGACATCC	202
QY	182	TGTCAACCACAATTCAGTATGGAAGCAAGGTATATGTCACACCCCTGCCGACATACCAG	241
Db	203	TGAGCCCCCAGTTCAGTACGCGCAGCAAGGTGTACGTGAAGCACCCCGGACATCCCG	262
QY	242	ACTATAAAAAGCTGTCAATTCCTGAAGGATTTAAATGGGAAAAGGTCATGAATTTGAAG	301
Db	263	ACTACAAGAAGCTGAGCTTCCCGAGGGCTTCAAGTGGAAGAGGGTGATGAATTCGAGG	322

QY	302	ACGGTGGCGTCGTTACTGTAAACCAGGATTCAGTTTGAGGATGGCTGTTTCATCTACA	361
Db	323	ACGGCGCGTGTGACCGGTGAACCAAGACAGCAGCCCTGCAGACGGCTGCTTCATCTACA	382
QY	362	AGGTCAAGTTCATTGGCGGTGAAC TTCTTCGANTGACCTGTATGCAAAAAGAACA	421
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QY	422	TGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTAGTGCGTGTGAAAGGAGAGA	481
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QY	542	ACATGGCAAGAAGCGCTGTGCAGCTACCAGGGTACTACTATGTTGACTCCAACTG	601
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QY	662	ACCATCTGTTCCTTAA	678
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LOCUS	AX370404	678 bp
DEFINITION	Sequence 1 from Patent WO0196373.	DNA
		linear
		PAT 16-FEB-2002

KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL
			1	Pradkov, A.F. and Terskikh, A.	synthetic construct synthetic construct artificial sequences.	
					Fluorescent timer proteins and methods for their use	
					Patent: WO 0196373-A 1 20-DEC-2001;	

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Best Local Similarity	78.9%;	Pred. No. 5.9e-122;		
Matches 535; Conservative	0;	Mismatches 143;	Indels 0;	Gaps 0;

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Db	61	ACCGTGAACGGCCACGAGTTTCGAGATCGAGGGCGAGGGCGGCGCCGCTTACGAGGGC	120
QY	121	CACAATACCCTAAAGCTTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGTCTGGGATATT	180
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QY	181	TTGTCAACCACAATTTCAGTATGGAAGCAAGTATATGTCAAGCACCTTGCCGACATACCA	240
Db	181	CTGTCCCCCAGTTCCAGTACGGCTCCCAAGGTGTACGTGAAGCACCCGCGCAGATCCCC	240
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Db 301 GACGGCGCGGTGTGACCGGTGACCTCAGGACTCTCCCTGCAGACGCGCTCTTCATCTAC 360

Qy 361 AAGGTCAAGTTCAATGGCGTGAATTCTCTCCGATGGACCCTGTTATGCAAAAGAAGACA 420

Db 361 AAGGTGAAGTTCAATCGCGTGAATCTCCCTCCGACGGCCCGTGAATGCAAAAGAAGACC 420

Qy 421 ATGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTATGCGCGTGTGAAAAGAGAG 480

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Db 541 TACATGGCCAAGAAGCCCGTGAAGCTGCCCCGCTACTACTACGTGGAATCCAAAGCTGGAC 600

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ACCESSION	AX824725				
VERSION	AX824725.1	GI:39750591			

SOURCE
ORGANISM
Discosoma sp.
Discosoma sp.
Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Coralimorpharia; Discosomatidae; Discosoma.

REFERENCE	1
AUTHORS	
TITLE	Non aggregating fluorescent proteins and methods for using the same
JOURNAL	Patent: WO 02068459-A 7 06-SEP-2002;
FEATURES	Location/Qualifiers
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Query Match	66.3%;	Score 449.2;	DB 6;	Length 678;
Best Local Similarity	78.9%;	Pred. No. 5.9e-122;		
Matches 535;	Conservative 0;	Mismatches 143;	Indels 0;	Gaps 0;

QY	1	ATGAGGCTTCCAGAATGTTATCAAGAGTTTCATGAGGTTTAAGTTTCATGGAAGGA	60
Db	1	ATGCGCTCTCCAGAAGACGTCATCAAGAGTTTCATGCGCTTCAAGGTCCGATGAGAGGC	60
QY	61	ACCGTCAATGGGCACGAGTTTGAATAAGAGCGGAAGGAGAGGGGACCATACGAAGGC	120
Db	61	ACCGTGAACGGCCACGAGTTTCAGATTCGAGGGCGAGGGCGAGGGCCGCCCTTACGAGGGC	120
QY	121	CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTGGCCATTGCTTGGATATT	180
Db	121	CACAACACCGTGAAGCTGAAGGTGACCAAGGGGGCCCTTGGCTTGGCTGGACATC	180
QY	181	TTGTCAACCACAATTTTCACTATGGAAGCAAGGTATATGTCAAGCAACCCTGCCGACATACCA	240
Db	181	CTGTCCCCCAGTTCAGTACGCGCTCCAAGGTGTACGTGAAGCACCCCGCGACATCCCC	240

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QY 241 GACTATAAAAAGCTGTCATTTCCTGAAGATTAAATGGGAAAGGTCATGACTTTGAA 300
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Db 301 GACGGCGGCGTGTGACCGTGAACCCAGGACTCTCCCTGCAGAGCGGTGTCATCTAC 360
QY 361 AAGGTCAAGTTCATTGGCGTGAACCTTCCGATGACCTGTATGCAAAAGAGACA 420
Db 361 AAGGTGAAGTTCATCGGCGTGAACCTTCCGACGCGCCCGTGATGACAGAGAGACC 420
QY 421 ATGGGCTGGAGAGCCAGCACTGAGCGGTTGTATCCTGCGATGCGCGTGTGAAGAGAG 480
Db 421 ATGGGCTGGAGAGCGCTCCAGCGGCGCTGTACCCCGCGAGCGCGTGTGAAGGCGAG 480
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Db 541 TACATGGCAAGAAGCGCGTGTGACGCTACCTACGTAAGTCAAGTCTGAC 600
QY 601 ATAACAAGCCACAAGAGACTATACAATGTTGACAGATGAAGAACCAGGAGCGC 660
Db 601 ATCACTCCCAACAAGAGACTACACCATCGTGAAGAGTACGAGCGCACCGAGGCGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 09:50:20 ; Search time 66 Seconds
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Searched: 682709 seqs, 277475446 residues

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	271	40.0	801	4 US-09-459-956-7	Sequence 7, Appli
4	178.4	26.3	690	4 US-09-459-956-2	Sequence 2, Appli
5	147.2	21.7	696	4 US-09-459-956-4	Sequence 4, Appli
6	133.4	19.7	696	4 US-09-459-956-3	Sequence 3, Appli
7	133.2	19.6	1079	4 US-09-609-161B-15	Sequence 15, Appli
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19	34.4	5.1	2748	4 US-09-540-236-1106	Sequence 1106, Ap
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ALIGNMENTS

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; Sequence 6, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459, 956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765, 860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481, 977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp
US-09-459-956-6

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QY	121	CACATACCGTAAGCTTAAAGTAACCAAGGGGACCTTGGCATTGCTGGATATT	180
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; Sequence 5, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 699
; TYPE: DNA
; ORGANISM: Discosoma striata
US-09-459-956-5
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Best Local Similarity 76.2%; Pred. No. 1.4e-131;
Matches 518; Conservative 0; Mismatches 159; Indels 3; Gaps 1;

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RESULT 3

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US-09-459-956-7
; Sequence 7, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 801
; TYPE: DNA
; ORGANISM: Clavularia sp
US-09-459-956-7
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Query Match 40.0%; Score 271; DB 4; Length 801;
Best Local Similarity 63.0%; Pred. No. 1.5e-83;
Matches 418; Conservative 0; Mismatches 245; Indels 0; Gaps 0;

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QY 71 GGCACGAGTTTGAATAGAGGCCAAGAGAGAGGGAGGCCATACGAAGCCACATACCG 130
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Db 425 TTGTCAAGTGAAGAAAGTGAACATAGCAATGAGAGAACTCCTTATCTATGAATTCGTT 484
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Db 545 AACCATCCACTGAGATTATGTACGTCGTGATGAGTGCTGGTCGAGAGATATTAGCCATT 604
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QY 491 CTCTGAAGTGAAGAACGGGTGTCTATTAACCTAGTTGAATTCAAAAGTATTACATGGCAA 550
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Db 605 CTCTGTGTGTGAGGAGGAGGTGGCCATTAACGATGTACTTCAAAAGTATTTACAAAGCAA 664
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 551 AGAAGCTGTGACGCTACCAAGGTACTACTATGTGACTCCAACTGATATTAACAAGCC 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 665 AAAAAGTGTCAAAATGGCCAGACTATCACTTTGTGACCATCGCATTTGAGATCTTGAACC 724
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 611 ACAAGAGACTATATCAATCGTTAGAGATGAAGAAGCAAGGAGGAGCCACCATCTGT 670
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 725 ATGACAAGATTACACAAGTAACGCTGTATGAGAATGACAGTTGCTCGCTATTCTTGC 784
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 671 TCC 673
    |||
Db 785 TGC 787
```

RESULT 4

```
US-09-459-956-2
; Sequence 2, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 690
; TYPE: DNA
; ORGANISM: Anemonia majano
US-09-459-956-2
```

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Query Match 26.3%; Score 178.4; DB 4; Length 690;
Best Local Similarity 56.1%; Pred. No. 1.6e-51;
Matches 360; Conservative 0; Mismatches 276; Indels 6; Gaps 1;
QY 9 TTCCAAGATGTATCAAGAGATTTCATGAGGTTTAAGTTGCGCATGGAAGAACGTCAT 68
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db 9 TTCAACAAGTTATCGAGATGACATGAATAATGACTACCATATGATGCGTGTCAA 68
QY 69 TGGGACAGATTGAAATAGAAGCGGAGAGAGAGGCGCATACGAAGCCACAATAC 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 69 TGGGCACTACTTACCCGTCAAAGGTGAAGGCAACGGGAGCCATACGAAGGAGCGAGAC 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 129 CGTAAAGCTTAAGTAA-----CCAAGGGGGACCTTTGCCATTGCTTGGATATTTT 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 129 TTGCACTTTTAAAGTACCATGCGCAACGCGTGGGCCCTTGCAATTCCTTTGACATACT 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 183 GTCAACCAATTTCAATGGAAGCAAGGTATATGTCAACCAACCCCTGCCGACATACCA 242
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 189 ATCTACAGTGTCAAAATATGGAATCGATGCTTACTGCGTATCTTACCAGTATGCCCGA 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 243 CTATAAAAAGCTGTCAATTTCTGAAAGATTAAATGGGAAAGGTCATGAACCTTTGAAGA 302
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 249 CTATTTCAACAAGCATTTCTGACGGAATGTCAATGAAGAAAGACTTTTACCTATGAAGA 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 303 CGGTGGCGTCTTAAGTAAACCCAGATTCCAGTTTGACAGATGGCTGTTTCACTTACAA 362
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 309 TGGAGAGTGTCTACAGCCAGTGGGAATAAGCCTTAAAGCAACTGCTTTGAGACAA 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 363 GGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGACCTGTATGCAAAAGAGACAAT 422
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 369 ATCCACGTTTCATGAGTGAACCTTCTGCTGATGACCTGTGATGGCGAAGAGACAAC 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 423 GGGCTGGGAAGCCAGCACTGAGCGTTGTATCTCTGATGAGCGGTGAAGAGAGAT 482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 429 TGGTTGGACCCATCTTTTGAAGAAATGACTGTCTGATGAGATATTTGAAGGTTGAT 488
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 483 TCATTAAGGCTCTGAAGCTGAAGACGGTGTCTATTAACCTAGTTGAATTCAAAAGTATTA 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 489 CACCGCTTCTCATGTCTGAAGAGAGGTGCAATTAAGATGCCAATTCACACTTCTTA 548
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 543 CATGGCAAGAAGCGCTGCACTACCAAGGTACTATGTTGACTCCAACTGATAT 602
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 549 CAAGACAAAAAACCGGTACGATGCCACCAACCATGTGTGGAACATCGCATTGGAG 608
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 603 AACAGCCACAACGAAGACTATATCAATCGTTGAGCAGTATGA 644
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 609 GACCGACCTTGACAAAGGTGGCAACAGTGTTCAGCTGACGGA 650
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 5

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US-09-459-956-4
; Sequence 4, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Zoanthus sp
US-09-459-956-4
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Query Match 21.7%; Score 147.2; DB 4; Length 696;
Best Local Similarity 56.8%; Pred. No. 1.1e-40;
Matches 316; Conservative 0; Mismatches 228; Indels 12; Gaps 2;
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OY 9 TTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGCAAGTCAA 68
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Db 9 TTCAAGCACCGTCTAAAGAAGAAATGACAAATGAATACACATGGAAGGTCGCTCAA 68
OY 69 TGGGCACGAGTTTGAATAAGAGCGGAAGGAGAGGGGACCATACGAAGGCCACAATAC 128
    |||||
Db 69 CGGACATAAATTGTGATCACGGCGGAGGCGATGGATATCCGTTCAAGGGAAACAGAC 128
OY 129 CGTAAAGCTTAAAGTAACCAAGGGGGGACCTTGGCATTGCTTGAGATTTTGTACC 188
    |||||
Db 129 TATTAATCTGTGTGATCGAAGGGGAGCACCATTTGCCATTTCCGAAGACATATGTGAGC 188
OY 189 ACAATTTCAGTATGAGCAAGGATATATGTCAAGCACCCCTGCCGACATACGACTATA 248
    |||||
Db 189 TGGCTTTAAGTACGAGACAGAGATTTTCACTGAATATCCTCAAGACATAGTACTATT 248
OY 249 AAAGCTGCATTTCTGTAAGGATTTAATGGGAAAGGTCATGACTTTGAAGCGTG- 307
    |||||
Db 249 CAAGAAGCTCGTCTGCTGGATATACATGGGGCAGGCTTTTCTCTTGAGATGAGC 308
OY 308 -----GCGTCGTTACTGTAAACCCAGGATTCAGTTTGCAGGATGGCTGTTCACTACAA 362
    |||||
Db 309 AGTCTGCATATGCATGTATGATATATAACAGTAGTGTCAAGAAAACTGCATTTATCATAA 368
OY 363 GGTCAAGTTCATTGGCGTGAACCTTCCCTCCGATGAGCCTGTATGCAAAAGAACAAAT 422
    |||||
Db 369 GAGCATATTTAATGAATGAATTTTCTGCTGATGACCTGTGATGAAGAAAGATGACAAC 428
OY 423 GGGCTGGGAAGCCAGCACTGACGTTT-----GTATCCTCGTATGGCGTGTGAAAGG 476
    |||||
Db 429 TAACTGGGAAGCATCTGCGAGAAGATCATGCGCATCTAAGCAGGGGATCTGAAAGG 488
OY 477 AGAGATTCAATAGGCTGTGAAGCTGAAGACGGTGTCACTTACCTAGTGAATCAAAAG 536
    |||||
Db 489 GGATGTCTCCATGTACCTCTTCTGAAGATGGTGGCGTTTACCGGTGCCAGTTGCAACAC 548
OY 537 TATTTACATGSCAAAG 552
    |||||
Db 549 AGTTTACAAAGCAAAG 564
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RESULT 6
US-09-459-956-3
; Sequence 3, Application US/09459956
; Patent No. 6342379
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Gonzalez, III, Jesus E.
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY
; TITLE OF INVENTION: OPTICAL METHODS
; FILE REFERENCE: REGEN1290-4
; CURRENT APPLICATION NUMBER: US/09/459,956
; CURRENT FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: 08/765,860
; PRIOR FILING DATE: 1999-05-08
; PRIOR APPLICATION NUMBER: 08/481,977
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: PCT/US96/09652
; PRIOR FILING DATE: 1996-06-06
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 696
; TYPE: DNA
; ORGANISM: Zoanthus sp
US-09-459-956-3
```

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Query Match 19.7%; Score 133.4; DB 4; Length 696;
Best Local Similarity 55.3%; Pred. No. 6.3e-36;
Matches 307; Conservative 0; Mismatches 236; Indels 12; Gaps 2;
OY 10 TCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTCCGATGGAAGCAAGCGTCAAT 69
    |||||
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Db 10 TCAAGCACCGTCTAACAAAAGAAATGACATGAATAACCGTATGGAAGGTGCGTCAT 69
OY 70 GGGCACGAGTTTGAATAGAGCGCAAGAGAGAGGGGAGGCCATACGAAGGCCACAATACC 129
    |||||
Db 70 GGACATAAATTGTGATCACGGGAGAGGGCATTTGGATATCCGTTCAAGGGAACAGGCT 129
OY 130 GTAAGCTTAAAGTAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATTTGTACCA 189
    |||||
Db 130 ATTAATCTGTGTGTGTCGAAGGTGACCATTTGCCATTTGCCGAAGACATATTTGACGCT 189
OY 190 CAATTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACGACTATAAA 249
    |||||
Db 190 GCCTTAACTACGGAACAGGGTTTCACTGAATATCCTCAAGACATAGTTGACTATTTC 249
OY 250 AAGCTGCATTTCTGTAAGGATTTAAATGGGAAAGGTCATGAACCTTGAAGACGG---- 305
    |||||
Db 250 AAGAAGCTCGTCTGCTGCTGATATACATGGGACAGGCTTTTCTCTTGAGATGAGCA 309
OY 306 --TGGCGTGTACTGTAAACCAAGATTCAGTTTGACAGATGGCTGTTCACTACAAAG 363
    |||||
Db 310 GTTGCATATGTAATGACAGATATAACAGTAGTGTGAAGAAACTGCATGTATCATGAG 369
OY 364 GTCAAGTTCATTGGCGTGAACCTTCTCCGATGAGACCTGTATGCAAAAGAACAAATG 423
    |||||
Db 370 TCCAATTTTATGAGTGAATTTTCTGCTGATGAGACCTGTGATGAAGAAAGATGACAGAT 429
OY 424 GGTGGGAAGCCAGCACTGACGTTT-----GTATCCTCGTATGGCGTGTGAAAGGA 477
    |||||
Db 430 AACTGGGAGCCATCTGCGAGAAGATCATACAGTACCTTAAAGCAGGGGATATTGAAAGGG 489
OY 478 GAGATTCATAGGCTCTGAAGCTGAAGAAGCGGTGTCACTTACCTAGTGAATCAAAAGT 537
    |||||
Db 490 GATGTCTCATGTACTCTTCTGTAAGATGGTGGCGTTTACCGGTGCCAATTCGACACA 549
OY 538 ATTTACATGSCAAAG 552
    |||||
Db 550 GTTTACAAAGCAAAG 564
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RESULT 7
US-09-609-161B-15
; Sequence 15, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC3
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIGH
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Renilla mulleri
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(975)
; OTHER INFORMATION: Renilla mulleri Green fluorescent Protein (GFP)
US-09-609-161B-15
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Query Match 19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

```

QY 13 AAGAATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGGAAGAAACGGTCAATGGG 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 AACACTGTGTTTACAAGAGTAATGTCGTATTAAGTAATCTGGAAGAAATTGTAACAAC 339
QY 73 CACGAGTTTGAATAGAAAGCGGAAGAGAGGAGGCCATACGAAGCCCAATACCGTA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 CATGTTTTCATCAATGAGGGTTGCGCAAGGAATATTTATTCGGCAATCAACTGGTT 399
QY 133 AAGCTTAAGGTAACCAAGGGGGACCTTGGCATTGCTTGGATATTTGTCAACCAAA 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 CAGATTCGTGCACGAAGGGGCCCACTGCTTTGCAATTTGATATTTGTCAACCACT 459
QY 193 TTTCAGTATGAAGCAAGGTATATGTCAAGCAACCCTGCCGACATACCACTATAAAAG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 TTTCATATGCGAACCCGACTTTCACGAATAATCCGATGATATATCAGATTATTTATA 519
QY 253 CTGTCAATTCCTGAAGATTTAATGGAAAGGGTCATGAACCTTGAAGACGGTGGCTC 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 CAATCATTTCCAGACAGGATTATGTATGAACGAACATTACGTTACGAAGATGGCGACTT 579
QY 313 GTTACTGTAAACCAGGATTCAGTTTGAAGATGGCTGTTTCATCTTACAAGTCAAGTTC 372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 GTTGAATTCGTTCAAGATATTAATTAATGAAGCAAGTTCGTTACAGAGTGAATAC 639
QY 373 ATTGGCGTGAACCTTCCCTCCAGTGAACCTGTATGCAAAAGAAAGCAATGGGCTGGAA 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 AAAGTAGTAACTTCCAGATGATGTCCTGTCATGCAAGACTATCTTAAGAATAGAG 699
QY 433 GCCAGCACTGAGCGTTGTATCCTCGTATGCGGTGTTGAAGAGAGATTCTAAGGCT 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CCTTCATTTGAAGCCATGTACATGAATAATGGCGTCTGTCGCGCAAGTAATCTTGTG 759
QY 493 CTGAAGCTGAAGACGGGTGTCATTAACCTAGTTGAATCAAAAGTAATTACATGGCAAG 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 TATAAATACTCTGGGAATATTAATGTCACATGAATAAATTAATGAAGTCGAAA 819
QY 553 AAGCCTGTGACCTAACAGGGTACTACTATGTGACTCCAACTGGATATAACAAGCCAC 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGTGTAGTAAAGAGTTTCTTCGTATCAATTTTATTCACACATCGTTTGAAGAAAGACTTAC 879
QY 613 AACGAAGACTATACAATCGTTGAGCAGTATGAAA 646
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 GTAGAAGACGGGGGTTCTGTTGAACAGCATGAGA 913

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RESULT 8
US-09-626-581D-64
; Sequence 64, Application US/09626581D

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; Patent No. 6548249
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
; FILE REFERENCE: A-66900-3/RMS
; CURRENT APPLICATION NUMBER: US/09/626,581D
; CURRENT FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 09/169,015
; PRIOR FILING DATE: 1998-10-08
; PRIOR APPLICATION NUMBER: 09/415,765
; PRIOR FILING DATE: 1999-10-08
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Renilla muelleri
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(975)

```

OTHER INFORMATION:
US-09-626-581D-64

Query Match 19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

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QY 13 AAGAATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGGAAGAAACGGTCAATGGG 72
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 AACACTGTGTTTACAAGAGTAATGTCGTATTAAGTAATCTGGAAGAAATTGTAACAAC 339
QY 73 CACGAGTTTGAATAGAAAGCGGAAGAGAGGAGGCCATACGAAGCCCAATACCGTA 132
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 CATGTTTTCATCAATGAGGGTTGCGCAAGGAATATTTATTCGGCAATCAACTGGTT 399
QY 133 AAGCTTAAGGTAACCAAGGGGGACCTTGGCATTGCTTGGATATTTGTCAACCAAA 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 CAGATTCGTGCACGAAGGGGCCCACTGCTTTTGCATTTGATATTTGTCAACCACT 459
QY 193 TTTCAGTATGAAGCAAGGTATATGTCAAGCAACCCTGCCGACATACCACTATAAAAG 252
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 TTTCATATGCGAACCCGACTTTCACGAATAATCCGATGATATATCAGATTATTTATA 519
QY 253 CTGTCAATTCCTGAAGATTTAATGGAAAGGGTCATGAACCTTGAAGACGGTGGCTC 312
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 CAATCATTTCCAGACAGGATTATGTATGAACGAACATTAACGTTACGAAGATGGCGACTT 579
QY 313 GTTACTGTAAACCAGGATTCAGTTTGAAGATGGCTGTTTCATCTACAAGTCAAGTTC 372
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 GTTGAATTCGTTCAAGATATTAATTAATGAAGCAAGTTCGTTACAGAGTGAATAC 639
QY 373 ATTGGCGTGAACCTTCCCTCCAGTGAACCTGTATGCAAAAGAAAGCAATGGGCTGGAA 432
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 AAAGTAGTAACTTCCAGATGATGTCCTGTCATGCAAGACTATCTTAAGAATAGAG 699
QY 433 GCCAGCACTGAGCGTTGTATCCTCGTATGCGGTGTTGAAGAGAGATTCTAAGGCT 492
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CCTTCATTTGAAGCCATGTACATGAATAATGGCGTCTGTCGCGCAAGTAATCTTGTG 759
QY 493 CTGAAGCTGAAGACGGGTGTCATTAACCTAGTTGAATCAAAAGTAATTACATGGCAAG 552
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 TATAAATACTCTGGGAATATTAATGTCACATGAATAAATTAATGAAGTCGAAA 819
QY 553 AAGCCTGTGACCTAACAGGGTACTATATGTGACTCCAACTGGATATAACAAGCCAC 612
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGTGTAGTAAAGAGTTTCTTCGTATCATTTTATTCACATCGTTTGAAGAAAGACTTAC 879
QY 613 AACGAAGACTATACAATCGTTGAGCAGTATGAAA 646
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 GTAGAAGACGGGGGTTCTGTTGAACAGCATGAGA 913

```

RESULT 9
US-09-415-765B-64
; Sequence 64, Application US/09415765B

```

; Patent No. 6548632
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; TITLE OF INVENTION: Fusions of Scaffold Proteins with Random Peptide
; FILE REFERENCE: A66900-1/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/415,765B
; CURRENT FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: 09/169,015
; PRIOR FILING DATE: 1998-10-08
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 64
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Renilla muelleri
; FEATURE:
; NAME/KEY: CDS

```



```
; LOCATION: (259)..(975)
; OTHER INFORMATION:
US-09-415-765B-64

Query Match      19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 13 AAGAATGTTATCAAGAGGTTTCATGAGTTTAAGTTTCGCATGGAAGGAACGGTCAATGGG 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 AACACTTGTTCACAGAGTAATGTCGTATTAAGTAATCTGGAAGGAATTGTAAACAAC 339

QY 73 CACGAGTTTGAATAGAGCGGAAGAGAGAGAGGAGCGCATACGAAGGCCACAATACCGTA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 CATGTTTTCACATGAGGGTTGCGGCAAGGGAATATTTATTCCGCAATCAACTGGTT 399

QY 133 AAGCTTAAGTAACCAAGGGGGACCTTTGCCATTGCTTGGATATTTTGTACCACAA 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 CAGATTCTGTACGAAGAGGGGGCCCACTGCCCTTTGCATTTGATATGTGTCAACCACT 459

QY 193 TTTCAGTATGAAGCAAGGTATATGTCAAGCAACCTGCCGACATACCAAGCTATAAAAG 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 TTTCATATGGAACCCGTAATTTCAAGAAATATCCGAATGATATATCAAGATTAATTTATA 519

QY 253 CTGTCAATTCCTGAAGATTAAATGGGAAAGGGTCACTTGAAGACGGTGGCGTC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 CAATCATTTCCAGCAGAGATTATGTATGAACGAACATTACGTTACGAAGATGGCGGACTT 579

QY 313 GTTACTGTAAACCAGATTCCAGTTTGCAAGATGGCTGTTTCATCTACAAAGTCAAGTTC 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 GTTGAATTCGTTCAAGATTAATAATTATAGAAACAAGTTCGTCTACAGAGTGAATAC 639

QY 373 ATTGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAAAGCAAACTGGGAA 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 AAAGTAGTAACCTCCAGATGATGTCGCCGTCAAGCAAGAACTATCTTAGAATAGAG 699

QY 433 GCCAGCACTGAGCGTTGTATCTCGTATGGCGTGTGAAGAGAGAGATTCATAAGCT 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CCTTCATTTGAAGCCATGTACATGAATAATGGCGTCTGTCGCGAAGTAATCTTGTTC 759

QY 493 CTGAAGCTGAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 TATTAACCTAAACTCTGGGAAATATTATTTCATGTCAATGAAAAACATTAAATGAACTCGAAA 819

QY 553 AAGCCTGTGACGTACCAAGGGTACTACTATGTGACTGCCAACTGGATATTAACAAGCCAC 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGTGTAGTAAAGAGTTTCCTTCGTATCATTTTATTCACATCGTTGGAAAAAGACTTAC 879

QY 613 AACGAAGACTATACAATCGTTGAGCAGTATGAAA 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 GTAGAAGACGGGGGTTGTTGAACAGCATGAGA 913

RESULT 10
US-09-626-580C-64
; Sequence 64, Application US/09626580C
; Patent No. 6562617
; GENERAL INFORMATION:
; APPLICANT: Anderson, David
; APPLICANT: Bogenberger, Jakob M.
; APPLICANT: Peele, Beau R.
; TITLE OF INVENTION: FUSIONS OF SCAFFOLD PROTEINS WITH RANDOM PEPTIDE LIBRARIES
; FILE REFERENCE: A-66900-2/RMS/AMS
; CURRENT APPLICATION NUMBER: US/09/626,580C
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: US 09/415,765
; PRIOR FILING DATE: 1999-10-08
; PRIOR APPLICATION NUMBER: US 09/169,015
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 1079
```

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; TYPE: DNA
; ORGANISM: Renilla muelleri
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(975)
; OTHER INFORMATION:
US-09-626-580C-64

Query Match      19.6%; Score 133.2; DB 4; Length 1079;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 13 AAGAATGTTATCAAGAGGTTTCATGAGTTTAAGTTTCGCATGGAAGGAACGGTCAATGGG 72
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 280 AACACTTGTTCACAGAGTAATGTCGTATTAAGTAATCTGGAAGGAATTGTAAACAAC 339

QY 73 CACGAGTTTGAATAGAGCGGAAGAGAGAGGAGCGCATACGAAGGCCACAATACCGTA 132
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 340 CATGTTTTCACATGAGGGTTGCGGCAAGGGAATATTTATTCCGCAATCAACTGGTT 399

QY 133 AAGCTTAAGTAACCAAGGGGGACCTTTGCCATTGCTTGGATATTTTGTACCACAA 192
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 400 CAGATTCTGTACGAAGAGGGGGCCCACTGCCCTTTGCATTTGATATGTGTCAACCACT 459

QY 193 TTTCAGTATGAAGCAAGGTATATGTCAAGCAACCTGCCGACATACCAAGCTATAAAAG 252
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 460 TTTCATATGGAACCCGTAATTTCAAGAAATATCCGAATGATATATCAAGATTAATTTATA 519

QY 253 CTGTCAATTCCTGAAGATTAAATGGGAAAGGGTCACTTGAAGACGGTGGCGTC 312
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 CAATCATTTCCAGCAGAGATTATGTATGAACGAACATTACGTTACGAAGATGGCGGACTT 579

QY 313 GTTACTGTAAACCAGATTCCAGTTTGCAAGATGGCTGTTTCATCTACAAAGTCAAGTTC 372
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 GTTGAATTCGTTCAAGATTAATAATTATAGAAACAAGTTCGTCTACAGAGTGAATAC 639

QY 373 ATTGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAAAGCAAACTGGGAA 432
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 AAAGTAGTAACCTCCAGATGATGTCGCCGTCAAGCAAGAACTATCTTAGAATAGAG 699

QY 433 GCCAGCACTGAGCGTTGTATCTCGTATGGCGTGTGAAGAGAGAGATTCATAAGCT 492
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 700 CCTTCATTTGAAGCCATGTACATGAATAATGGCGTCTTGGTCGCGAAGTAATCTTGTTC 759

QY 493 CTGAAGCTGAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG 552
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 TATTAACCTAAACTCTGGGAAATATTATTTCATGTCAATGAAAAACATTAAATGAACTCGAAA 819

QY 553 AAGCCTGTGACGTACCAAGGGTACTACTATGTGACTGCCAACTGGATATTAACAAGCCAC 612
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 820 GGTGTAGTAAAGAGTTTCCTTCGTATCATTTTATTCACATCGTTGGAAAAAGACTTAC 879

QY 613 AACGAAGACTATACAATCGTTGAGCAGTATGAAA 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 880 GTAGAAGACGGGGGTTGTTGAACAGCATGAGA 913

RESULT 11
US-09-277-716-15
; Sequence 15, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
```


EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 15
; LENGTH: 1079
; TYPE: DNA
; ORGANISM: Renilla mulleri
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (259)..(975)
; FEATURE:
; OTHER INFORMATION: Renilla mulleri Green Fluorescent Protein (GFP)
US-09-277-716-15

Query Match 19.6%; Score 133.2; DB 3; Length 1085;
Best Local Similarity 50.6%; Pred. No. 9.7e-36;
Matches 321; Conservative 0; Mismatches 313; Indels 0; Gaps 0;

QY 13 AAGATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGGAAGAACGTCATGGG 72
DB 280 AACACTGTGTTTACAAGAGTAATGTCGTATTAAGTAATCTGGAAGGAATGTAACAAC 339
QY 73 CACGAGTTGAAATAGAAAGCGGAAGAGAGGAGCCCATACGAAGCCCAATACCGTA 132
DB 340 CATGTTTATCAATGAGAGGTGCGGCAAGGAATATTTATTCCGCAATCAACTGTT 399
QY 133 AAGCTTAAGTAACCAAGGGGGGACCTTGGCATTGCTTGGGATATTTGTCAACCAAA 192
DB 400 CAGATTCGTGTCAGAAAGGGGCCCCCACTGCTTTTGCAATTGATATTTGTCAACCACT 459
QY 193 TTTCAGTATGAGCAAGATATATGTCAAGCAACCTGCGACATACCACTATAAAAG 252
DB 460 TTTCATATGCAACCGTACTTTCACGAATATCCGAATGATATATCAGATTTATTTATA 519
QY 253 CTGTCAATTCCTGAAGATTTAATGGGAAGGTCATGAACCTTGAAGACGGTGGCTC 312
DB 520 CAATCATTTCCAGCAGAGATTATGTATGAAGAACATTAACGTTACGAGATGGCGACTT 579
QY 313 GTTACTGTAAACCAAGATTCAGTTTGCAGATGGCTGTTTCATCTACAGTCAAGTTC 372
DB 580 GTTGAATTCGTTCAAGATTAATTAATTAAGAACAAAGTTCGTTACAGAGTGAATAC 639
QY 373 ATTGGCGTGAACCTTCTCCGATGAGCCTGTTATGCAAAAGAAAGCAATGGGCTGGAA 432
DB 640 AAAGTAGTAACTTCCAGATGATGTCCTGATGACAGAGACTATCTTAAGAAATAGAG 699
QY 433 GCCAGCACTAGCGTTTGTATCCTGATGAGCGTGTGAAGAGAGATTCATAAGCT 492
DB 700 CCTTCATTTGAAGCCATGTACATGAATTAAGCGCTTGTGCGGAGTAATCTTGTG 759
QY 493 CTGAAGCTGAAGACGGTGTCTATTAACCTAGTTGAATTCAAAAGTAATTACATGGCAAG 552
DB 760 TATAAATACTCTGGGAATATTAATTCATGTCACATGAAGAAACATTAATGAAGTCGAA 819
QY 553 AAGCCTGTGCACTAACAGGGTACTACTATGTGACTCCAACTGGATATAACAAGCCAC 612
DB 820 GGTGTAGTAAAGAGTTTCTTCGTATCAATTTTATTCAACATCGTTGGAAGAAAGACTTAC 879
QY 613 AACGAAGACTATACATCGTTGAGCAGTATGAAA 646
DB 880 GTAGAAGACGGGGGTTGTTGAACAGCATGAGA 913

RESULT 12
US-09-277-716-30
; Sequence 30, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE
; CURRENT APPLICATION NUMBER: US/09/277,716A

CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; FEATURE:
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-277-716-30

Query Match 19.5%; Score 132.4; DB 3; Length 1104;
Best Local Similarity 50.3%; Pred. No. 1.9e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 13 AAGATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGGAAGAACGTCATGGG 72
DB 55 AACACTGACTGAAGAGATTAATGTCGCAAAAGCTAGCGTTGAAGGAATCGTAACAAT 114
QY 73 CACGAGTTGAAATAGAAAGCGGAAGAGAGGAGGCAATACGAAGCCCAATACCGTA 132
DB 115 CACGTTTTCATGAGAGATTGGAAGCAATGATTAATTTGGAACCAATTGATG 174
QY 133 AAGCTTAAGTAACCAAGGGGACCTTGGCATTGCTTGGGATATTTGTCAACCAAA 192
DB 175 CAATCCGGGTACAAAGGGAGTCCGTTGCCATTGCTTGCATATTTGTTCCATAGCT 234
QY 193 TTTCAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCCACATACCACTATAAAAG 252
DB 235 TTCCAATACGGGAATCGCACTTTCACGAATATACCAAGACATTCGCGACTACTTGT 294
QY 253 CTGTCAATTCCTGAAGATTTAATGGGAAGGTCATGAACCTTGAAGACGGTGGCTC 312
DB 295 CAATCATTTCCCGCTGATTTTCTACGAAGAAATCTACGCTTTGAAGATGGCGCAAT 354
QY 313 GTTACTGTAAACCAAGATTCAGTTTGCAGATGGCTGTTTCATCTACAAAGTCAAGTTC 372
DB 355 GTTGACATTCGTTCAAGATTAATTAAGAGATGATTAAGTCACTACAAAGTGAGTAT 414
QY 373 ATTGGCGTGAACCTTCTCCGATGAGCCTGTTATGCAAAAGAAACAATGGGCTGGAA 432
DB 415 AGAGCAACGGTTTCCCTAGTAAGGACCCGATGAGCAAAAGCCATCCTCGCATGAG 474
QY 433 GCCAGCACTAGCGTTTGTATCCTGATGAGCGTGTGAAGAGAGATTCATAAGCT 492
DB 475 CCATCGTTTGAGGTGCTACATGAACAGCGGCTTCTGTTGGGCGAAGTAGATCTGCT 534
QY 493 CTGAAGCTGAAGACGGTGTCTATTAACCTAGTTGAATTCAAAAGTAATTACATGGCAAG 552
DB 535 TACAACTCGAGTACGGGAATTAATCTGTCGCCACATGAAAGCGTTTACAGATCCAAA 594
QY 553 AAGCCTGTGCACTAACAGGGTACTACTATGTGACTCCAACTGGATATAACAAGCCAC 612
DB 595 GGTGAGTGAAGAAATTCGGAATATCACTTATCATCATCTGCTGAGAGAAACCTTAC 654
QY 613 AACGAAGACTATACATCGTTGAGCAGTATGAAAAGAACGAGGAG 658
DB 655 GTGAAGAAAGAGCTTGTGGAACAACAGAGACGGCCATTGCAC 700

RESULT 13
US-09-609-161B-30
; Sequence 30, Application US/09609161B
; Patent No. 6436682

```
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 30
; LENGTH: 1104
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(747)
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert A)
US-09-609-161B-30
```

```
Query Match      19.5%; Score 132.4; DB 4; Length 1104;
Best Local Similarity 50.3%; Pred. No. 1.9e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 13 AAGAATGTATCAAGAGTTCATGAGTTTAAGTTGCATGGAAGAACGTCATGGG 72
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 55 AACACTGGAAGTGAAGATTAATGTCGCGAAGAGCTAGCGTTGAAGATCGTGAACAAT 114

QY 73 CACGAGTTGAATAGAGCGGAGAGAGAGAGGAGGCCATACGAAGGCCACAATACCGTA 132
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 115 CACGTTTTCATGGAAGATTTGAAAAAGGCAATGTAATTATTGAAACCAATTGATG 174

QY 133 AAGCTTAAGTAACCAAGGGGGACCTTTGCCATTGCTTGGGATATTTGTCCACCA 192
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 175 CAAATCCGGGTTACAAGGGAGGTCGTTGCCATTGCTTGCATATTGTTCCATAAGCT 234

QY 193 TTTCAGTATGAAGCAAGGTATATGTCAGACCCCTGCCGACATACAGACTATAAAAA 252
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 235 TTCCAATACGGGAATCGCACTTTCAGGAATACCCAGACGACATTGCCGACTACTTTGTT 294

QY 253 CTGTCATTTCCTGAAGATTAAATGGAAAGGGTCATGAACCTTTGAAGACGCTGCGTC 312
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 295 CAATCATTTCCCGCTGATTTTCTACGAAGAATAATCAGCTTTGAAGATGGCGCATTT 354

QY 313 GTTACTGTAACCCAGATTCAGTTTGCAGATGGCTGTTTCATCTACAAGTCAAGTTC 372
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 355 GTTGACATTGCTTCAGATATAAGTTTGAAGATGATTAAGTTCCACTACAAAGTGAGTAT 414

QY 373 ATTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAAGACAATGGCGTGGAA 432
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 415 AGAGGCAACGGTTTCCCTAGTAACGGAACCCGTCATGCAAAAAGCCATCTCGGATGGAG 474

QY 433 GCCAGCACTGAGCGTTTGTAATCTCTGTCATGGCGCTGTTGAAGAGAGAGATTCAATAGGCT 492
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 475 CCATCGTTTGAAGTGTCTACATGAACAGCGCGCTTCGTGGGCGAAGTACATCTCGTT 534

QY 493 CTGAAGCTGAAGACGGTGTGATTAACCTAGTTGAATCAAAAAGTATTATTCATGGCAAG 552
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 535 TACAACACTCGAGTCAAGGAATTAATCTCGTCCACATGAAAAAGCTTTTACAGATCCAAA 594

QY 553 AAGCCTGTGAGCTACAGGGTAATCTATGTTGATCCAAACTGATATATAAGCCAC 612
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 595 GGTGAGTGAAGAATTCGCCGATATCACTTTATCCATCATCGTCTGAGAAAAACCTAC 654
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QY 613 AACGAGCTATACAATCGTTGAGCAGTATGAAGAACCAGGAGC 658
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 655 GTGAAGAAGAACTTCGTGAACACACGAGACGGCCATTGCAC 700

RESULT 14
US-09-277-716-31
; Sequence 31, Application US/09277716A
; Patent No. 6232107
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; CURRENT APPLICATION NUMBER: US/09/277,716A
; CURRENT FILING DATE: 1999-03-26
; EARLIER APPLICATION NUMBER: 60/102,939
; EARLIER FILING DATE: 1998-10-01
; EARLIER APPLICATION NUMBER: 60/089,367
; EARLIER FILING DATE: 1998-06-15
; EARLIER APPLICATION NUMBER: 60/079,624
; EARLIER FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert B)
US-09-277-716-31
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```
Query Match      19.5%; Score 132.4; DB 3; Length 1279;
Best Local Similarity 50.3%; Pred. No. 2e-35;
Matches 325; Conservative 0; Mismatches 321; Indels 0; Gaps 0;

QY 13 AAGAATGTATCAAGAGTTCATGAGTTTAAGTTGCATGGAAGAACGTCATGGG 72
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 28 AACACTGGAAGTGAAGATTAATGTCGCGAAGAGCTAGCGTTGAAGATCGTGAACAAT 87

QY 73 CACGAGTTGAATAGAGCGGAGAGAGAGGAGGCCATACGAAGGCCACAATACCGTA 132
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 88 CACGTTTTCATGGAAGATTTGAAAAAGGCAATGTAATTATTGAAACCAATTGATG 147

QY 133 AAGCTTAAGTAACCAAGGGGGACCTTTGCCATTGCTTGGGATATTTGTCAACCA 192
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 148 CAAATCCGGGTTACAAGGGAGGTCGTTGCCATTGCTTGCATATTGTTCCATAGCT 207

QY 193 TTTCAGTATGAAGCAAGGTATATGTCAGACCCCTGCCGACATACAGACTATAAAAA 252
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 208 TTCCAATACGGGAATCGCACTTTCAGGAATAACCCAGACGACATTCGCACTACTTGT 267

QY 253 CTGTCATTTCCTGAAGATTAAATGGAAAGGGTCATGAACCTTTGAAGACGCTGCGTC 312
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 268 CAATCATTTCCCGCTGATTTTCTACGAAGAATAATCAGCTTTGAAGATGGCGCATTT 327

QY 313 GTTACTGTAACCCAGATTCAGTTTGCAGATGGCTGTTTCATCTACAAGTCAAGTTC 372
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 328 GTTGACATTGCTTCAGATATAAGTTTGAAGATGATTAAGTTCCACTACAAAGTGAGTAT 387

QY 373 ATTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAAGACAATGGCGTGGAA 432
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 388 AGAGGCAACGGTTTCCCTAGTAACGGAACCGTCATGCAAAAAGCCATCTCGGATGGAG 447

QY 433 GCCAGCACTGAGCGTTTGTAATCTCTGTCATGGCGCTGTTGAAGAGAGATTCATAAGGCT 492
   |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 448 CCATCGTTTGAAGTGTCTACATGAACAGCGCGTCTGTGGGCGAAGTATCTCGTT 507

QY 493 CTGAAGCTGAAGACGGTGTGTCATTACCTAGTTGAATTCAAAAAGTATTACATGGCAAG 552
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Db 508 TACAACCTCGAGTCAGGAACTATTACTCGTGCCACATGAAGCGTTTACAGATCCAAA 567

QY 553 AAGCCTGTGACGTAACAGGGTACTACTATGTGACTCCAACCTGGATATACAAGCCAC 612

Db 568 GGTGAGTGAAGAATTTCCCGGAATATCACTTTATTCATCATCGTCTGGAGAAACCTAC 627

QY 613 AACGAAGCTATACAAATCGTTGAGCAGTATGAAAGAACCGAGGGAC 658

Db 628 GTGAAGAAGGAGCTTCGTGGAACACACAGAGCGGCCATTGCAC 673

RESULT 15

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US-09-609-161B-31
; Sequence 31, Application US/09609161B
; Patent No. 6436682
; GENERAL INFORMATION:
; APPLICANT: Bryan, Bruce
; APPLICANT: Szent-Gyorgyi, Christopher
; APPLICANT: PROLUME, LTD.
; TITLE OF INVENTION: LUCIFERASES, FLUORESCENT PROTEINS, NUCLEIC ACIDS ENCODING THE LUC
; TITLE OF INVENTION: AND FLUORESCENT PROTEINS AND THE USE THEREOF IN DIAGNOSTICS, HIG
; TITLE OF INVENTION: SCREENING AND NOVELTY ITEMS
; FILE REFERENCE: 24729-121B
; CURRENT APPLICATION NUMBER: US/09/609,161B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/277,716
; PRIOR FILING DATE: 1999-03-26
; PRIOR APPLICATION NUMBER: 60/102,939
; PRIOR FILING DATE: 1998-10-01
; PRIOR APPLICATION NUMBER: 60/089,367
; PRIOR FILING DATE: 1998-06-15
; PRIOR APPLICATION NUMBER: 60/079,624
; PRIOR FILING DATE: 1998-03-27
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 31
; LENGTH: 1279
; TYPE: DNA
; ORGANISM: Ptilosarcus gurneyi
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (7)..(720)
; OTHER INFORMATION: Ptilosarcus Green Fluorescent Protein (GFP) (insert B)
US-09-609-161B-31

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Query Match	19.5%	Score 132.4;	DB 4;	Length 1279;
Best Local Similarity	50.3%;	Pred. No. 2e-35;		
Matches 325; Conservative	0;	Mismatches 321;	Indels 0;	Gaps 0;

OY		13	AAGAATGTTATCAAGGAGTTCATGAGCTTTAAAGSTTCCATGTGAAGCAACGGTCAAATGGG	72
Db		28	AACA CTG GACTG AAAAGAGATTATGTGCGC AAAAAAGCTA GC GTTG AAAGGAATCGTGA CAAT	87
OY		73	CACGAGTTTGAATAGAAAGGCCAAAGAGAGGGAGGCCATACGAAGGCCACAATACCGTA	132
Db		88	CACG TTTT TTCCATG GAAGGATTTGAAAAGCCAATGTATTATTGGA AACCAATTGATG	147
OY		133	AAGCTTAAGGTAACCAAGGGGGGACCTTGCCATTGTGCTTGGATATTTGTCA CACA CA	192
Db		148	CAATATCCGGGTTACA AAGGAGGTCCGTTGCCATTGCCTTTCGACATTTGTTCCATA GCT	207
OY		193	TTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACCAGACTATAAAAAG	252
Db		208	TTCCAATACGGGAATCGCACTTTCACGAAATAACCCAGACGACATTTGCCGACTACTTTGTT	267
OY		253	CTGTCAATTTCTGAAAGGATTTAAATGGGAAAAGGTCATGAACCTTGAAGACGGTGGCGTC	312
Db		268	CAATCATTTTCCGGCTG GATTTTTCTACGAAAAGAAATCTACGCTTTGAAGATGGCGCATTT	327
OY		313	GTTACTGTAAACCAGGATTCAGTTTGCAAGATGGCTGTTTCATCTTACAAGGTCAAGTTC	372
Db		328	GTTGACATTCGTTCA GATATAAGTTTAGAGATGATPAAGTTCCACTACAAAGTGAGAT	387

QY 373 ATTGGCGTGAACCTTTCCTCCGATGGAACCTGTTATGCAAAAGAAAGACAAATGGCGTGGAA 432

Db 388 AGAGGCAACGGTTTCCTTAGTAAAGGACCCCGTATGCAAAAAGCCATCCTCGGCATGGAG 447

QY 433 GCCAGCAGTGAAGCGTTTGTAATCCTCGTATGCGCGTGTGAAAGAGAGATTCAAAAGCT 492

Db 448 CCATCGTTTGAAGTGGTCAATGAACAAGCGCGTTCGTGGGCGAAGTAGATCTCGTT 507

QY 493 CTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATTTCATGCGCAAAG 552

Db 508 TACAACCTCGAGTCAGGGAACATACTCTGTCGCACATGAAAAAGTTTACAGATCCAAA 567

QY 553 AAGCCTGTGAGCTAACCAAGGTAATACTATGTTGACTCCAAACTGGAATATAACAAGCCAC 612

Db 568 GGTGAGTGAAGAATTCGCCGAATATCACTTTATCCATCATCCTCTGGAAGAAAACCTAC 627

QY 613 AACGAAGACTATACAATCGTTGAGCAGTATGAAAGAACCGAGGAC 658

Db 628 GTGGAAGAGAAGCTTCGTGGAACAACACAGAGACGCCATTGCAAC 673

Search completed: July 11, 2004, 11:16:48
Job time : 68 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: July 8, 2004, 09:54:11 ; Search time 50 Seconds
(without alignments)
1403.632 Million cell updates/sec

Title: US-10-006-922A-12
Perfect score: 1214
Sequence: 1 MRSSKNVKEFMRFKVRMEG.....EDYTIQEYERTEGRHHLFL 225

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1279676 seqs, 311918243 residues
Total number of hits satisfying chosen parameters: 1279676

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1214	100.0	225	9	US-09-999-745-67 Sequence 67, Appl
2	1214	100.0	225	10	US-09-866-538-12 Sequence 12, Appl
3	1214	100.0	225	10	US-09-794-308-12 Sequence 12, Appl
4	1214	100.0	225	10	US-09-865-291-12 Sequence 12, Appl
5	1214	100.0	225	12	US-10-132-067-4 Sequence 4, Appli
6	1214	100.0	225	13	US-10-006-922-12 Sequence 12, Appl
7	1214	100.0	225	14	US-10-081-864-8 Sequence 8, Appli
8	1214	100.0	225	14	US-10-121-258-1 Sequence 1, Appli
9	1214	100.0	225	14	US-10-315-920-2 Sequence 56, Appl
10	1214	100.0	225	15	US-10-370-570-56 Sequence 32, Appl
11	1214	100.0	225	15	US-10-406-618-32 Sequence 13, Appl
12	1214	100.0	487	15	US-10-433-640-13 Sequence 2, Appli
13	1214	100.0	487	15	US-10-343-977-1 Sequence 1, Appli
14	1214	100.0	506	15	US-10-343-977-2 Sequence 3, Appli
15	1214	100.0	547	15	US-10-343-977-3 Sequence 3, Appli

16	1210	99.7	240	14	US-10-152-296-2	Sequence 2, Appli
17	1210	99.7	240	16	US-10-739-656-2	Sequence 2, Appli
18	1210	99.7	545	14	US-10-214-932-52	Sequence 52, Appl
19	1210	99.7	548	14	US-10-214-932-76	Sequence 76, Appl
20	1207	99.4	225	14	US-10-121-258-20	Sequence 20, Appl
21	1207	99.4	225	14	US-10-315-920-4	Sequence 4, Appli
22	1196	98.5	236	16	US-10-314-936-2	Sequence 2, Appli
23	1196	98.5	236	16	US-10-314-936-4	Sequence 4, Appli
24	1191	98.1	225	14	US-10-315-920-6	Sequence 6, Appli
25	1186	97.7	225	15	US-10-442-148A-7	Sequence 7, Appli
26	1186	97.7	239	15	US-10-442-148A-8	Sequence 8, Appli
27	1160	95.6	225	14	US-10-121-258-4	Sequence 4, Appli
28	1153	95.0	225	14	US-10-121-258-24	Sequence 24, Appl
29	1132	93.2	225	16	US-10-423-688A-41	Sequence 41, Appl
30	1121	92.3	226	14	US-10-121-258-6	Sequence 6, Appli
31	1119	92.2	225	13	US-10-006-922-44	Sequence 44, Appl
32	1119	92.2	225	13	US-10-081-864-12	Sequence 12, Appl
33	1085.5	89.4	230	13	US-10-006-922-18	Sequence 18, Appl
34	1085.5	89.4	230	14	US-10-161-403-40	Sequence 40, Appl
35	1046	86.2	205	13	US-10-006-922-46	Sequence 46, Appl
36	1021	84.1	225	14	US-10-121-258-8	Sequence 8, Appl
37	765	63.0	227	13	US-10-006-922-10	Sequence 10, Appl
38	729.5	60.1	232	14	US-10-133-973-5	Sequence 5, Appli
39	729.5	60.1	232	15	US-10-370-570-64	Sequence 64, Appl
40	690	56.8	225	15	US-10-370-570-61	Sequence 61, Appl
41	681	56.1	225	14	US-10-244-779-2	Sequence 2, Appli
42	680.5	56.1	227	14	US-10-314-827-4	Sequence 4, Appli
43	680.5	56.1	227	14	US-10-314-827-6	Sequence 6, Appli
44	680.5	56.1	227	14	US-10-314-827-8	Sequence 8, Appli
45	680.5	56.1	227	14	US-10-314-827-10	Sequence 10, Appl

ALIGNMENTS

RESULT 1
US-09-999-745-67
Sequence 67, Application US/09999745
Patent No. US20020157120A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Tsien, Roger Y.
APPLICANT: Baird, Geoffrey
TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
FILE REFERENCE: REGEN1470-1
CURRENT APPLICATION NUMBER: US/09/999,745
CURRENT FILING DATE: 2001-10-23
PRIOR APPLICATION NUMBER: 09/316,920
PRIOR FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 67
SOFTWARE: PatentIn version 3.0
SEQ ID NO 67
LENGTH: 225
TYPE: PRT
ORGANISM: Discosoma sp.
US-09-999-745-67

Query Match	100.0%	Score 1214;	DB 9;	Length 225;
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QY	121	KYKFIGVNFPSDGPVWQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYVPEFSI	180	
DB	121	KYKFIGVNFPSDGPVWQKKTGWGEASTERLYPRDGLKGEIHKALKKDGGHYVPEFSI	180	

QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225

RESULT 2

US-09-866-538-12
; Sequence 12, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEH, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-866-538-12

Query Match 100.0%; Score 1214; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LSPQFGYSKVVYVADIPDYKLSFPEGFKWERNVNFEDGCVTTQDSSLQDGCFTY 120
Db 61 LSPQFGYSKVVYVADIPDYKLSFPEGFKWERNVNFEDGCVTTQDSSLQDGCFTY 120
QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225

RESULT 3

US-09-794-308-12
; Sequence 12, Application US/09794308
; Publication No. US20030170911A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEH, Roger
; APPLICANT: ZACHARIAS, David
; APPLICANT: BAIRD, Geoffrey
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530
; CURRENT APPLICATION NUMBER: US/09/794,308
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-794-308-12

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Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 LSPQFGYSKVVYVADIPDYKLSFPEGFKWERNVNFEDGCVTTQDSSLQDGCFTY 120
QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225

RESULT 4

US-09-865-291-12
; Sequence 12, Application US/09865291
; Publication No. US20030186229A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIEH, Roger
; APPLICANT: TING, Alice
; APPLICANT: ZHANG, Jin
; TITLE OF INVENTION: EMISSION RATIONETRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: REGEN1550
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-09-865-291-12

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Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 LSPQFGYSKVVYVADIPDYKLSFPEGFKWERNVNFEDGCVTTQDSSLQDGCFTY 120
Db 61 LSPQFGYSKVVYVADIPDYKLSFPEGFKWERNVNFEDGCVTTQDSSLQDGCFTY 120
QY 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
Db 121 KVKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKKDGHYLVEFKSI 180
QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225
Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTYVEQYERTEGRHHLFL 225

RESULT 5

US-10-132-067-4
; Sequence 4, Application US/10132067
; Publication No. US20030203355A1
; GENERAL INFORMATION:
; APPLICANT: Bradbury, Andrew
; APPLICANT: Zeytun, Ahmet
; APPLICANT: Waldo, Geoffrey
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fluorescence
; FILE REFERENCE: 021362-000600US
; CURRENT APPLICATION NUMBER: US/10/132,067
; CURRENT FILING DATE: 2002-04-24
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1

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; SEQ ID NO 4
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
; FEATURE:
; OTHER INFORMATION: red fluorescent protein (dsRED)
US-10-132-067-4
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Best Local Similarity 100.0%; Pred. No. 1.6e-120;
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QY 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
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QY 181 YMAKKEPVQLPGYYVVDISKDITSHNEDYTIIVEQYERTEGRHHLFL 225
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RESULT 6

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US-10-006-922-12
; Sequence 12, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yulii A.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Teretikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US/10/006,922
; CURRENT FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 09/120,330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457,898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,144
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma species
US-10-006-922-12
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Query Match          100.0%; Score 1214; DB 13; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVTKLKVTKGGPLPFAWDI 60

QY 61 LSPQFGYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNPFEDGGVTVTQDSSLQDGCFTY 120
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DB 61 LSPQFGYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNPFEDGGVTVTQDSSLQDGCFTY 120
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QY 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
    |||||||
DB 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180

QY 181 YMAKKEPVQLPGYYVVDISKDITSHNEDYTIIVEQYERTEGRHHLFL 225
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DB 181 YMAKKEPVQLPGYYVVDISKDITSHNEDYTIIVEQYERTEGRHHLFL 225
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RESULT 7

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US-10-081-864-8
; Sequence 8, Application US/10081864
; Publication No. US20030022287A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey
; APPLICANT: Lukyanov, Konstantin
; APPLICANT: Yanushevich, Yuriy
; APPLICANT: Savitsky, Alexandr
; APPLICANT: Fradkov, Arcady
; TITLE OF INVENTION: No. US20030022287A1 Aggregating Fluorescent Proteins and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-067
; CURRENT APPLICATION NUMBER: US/10/081,864
; CURRENT FILING DATE: 2002-06-19
; PRIOR APPLICATION NUMBER: 10/006,922
; PRIOR FILING DATE: 2001-12-04
; PRIOR APPLICATION NUMBER: 60/270,983
; PRIOR FILING DATE: 2001-02-21
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-081-864-8
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Query Match          100.0%; Score 1214; DB 14; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.6e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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    |||||||
DB 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGGRPYEGHNTVTKLKVTKGGPLPFAWDI 60

QY 61 LSPQFGYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNPFEDGGVTVTQDSSLQDGCFTY 120
    |||||||
DB 61 LSPQFGYGSKYVVKHPADIPDYKKLSFPEGFKMERVMNPFEDGGVTVTQDSSLQDGCFTY 120

QY 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180
    |||||||
DB 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKLKDGGHYLVEFKSI 180

QY 181 YMAKKEPVQLPGYYVVDISKDITSHNEDYTIIVEQYERTEGRHHLFL 225
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DB 181 YMAKKEPVQLPGYYVVDISKDITSHNEDYTIIVEQYERTEGRHHLFL 225
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RESULT 8

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US-10-121-258-1
; Sequence 1, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CPI
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
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; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(225)
; OTHER INFORMATION: wild-type DsRed
US-10-121-258-1

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Query Match	100.0%;	Score 1214;	DB 14;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.6e-120;		
Matches 225;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKKLVTKGGRPLPFAWDI 60
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1 MRSSKNVKEFMRFKVRMEGTVNGHEFEIEGEGEGRPYEGHNTVKKLVTKGGRPLPFAWDI 60

[illegible]

Qy 121 KVKFI GVNFP S DGPVMÖKKT MGWEASTERLYPRDGLV LKGEIHKAL KLKDGGHYLV EFKSI 180
|||
Db 121 KYEFI GVNFP S DGPVMÖKKT MGWEASTERLYPRDGLV LKGEIHKAL KLKDGGHYLV EFKSI 180

[illegible]

RESULT 9
US-10-31

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; Sequence 2, Application US/10315920
; Publication No. US20030175809A1
; GENERAL INFORMATION:
; APPLICANT: Fradkov, Arcady Fedorovich
; APPLICANT: Teresikh, Alexey
; TITLE OF INVENTION: FLUORESCENT TIMER PRO
; TITLE OF INVENTION: FOR THEIR USE
; FILE REFERENCE: CLON-077CIP
; CURRENT APPLICATION NUMBER: US/10/315,920
; CURRENT FILING DATE: 2002-12-09
; PRIOR APPLICATION NUMBER: 60/211,607
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: PCT/US01/19097
; PRIOR FILING DATE: 2001-06-13
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-315-920-2

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Query Match	100.0%;	Score 1214;	DB 14;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.6e-120;		
Matches 225; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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QY 121 KVKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGLKEIHKALKLKDGHYLVFCKSI 180

Db 121 KYKFIGVNFPSDGPVMQKKTMGWEASTERLYPRDGLKGEIHKALKKDGSHLVFEKSI 180

QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

Db 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIVEQYERTEGRHHLFL 225

RESULT 10
US-10-370

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; Sequence 56, Application US/10370570
; Publication No. US20030219717A1
; GENERAL INFORMATION:
; APPLICANT: DAHL, Soren Weis et al.
; TITLE OF INVENTION: FLUOROPHORE COMPLEMENTATION PRODUCTS
; FILE REFERENCE: 3759-0130P
; CURRENT APPLICATION NUMBER: US/10/370,570
; CURRENT FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Discosoma sp.
US-10-370-570-56

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Query Match	100.0%;	Score 1214;	DB 15;	Length 225;
Best Local Similarity	100.0%;	Pred. No. 1.6e-120;		
Matches 225; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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Qy	121	KVAFIGVNFPSPDGPVMOKKTMGWEASTERLYPRDGLKGEIHKALK.KDGGHYLVEFKSI	180
Db	121	KYKFIGNVPSPDGPVMOKKTMGWEASTERLYPRDGLKGEIHKALK.KDGGHYLVEFKSI	180

QY 181 YMAKKPVQLPGYYVDSKLDITSHNEDYTIIVEQYERTEGRHLLFL 225
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RESULT 11
US-10-406-618-32

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; Sequence 32, Application US/10406618
; Publication No. US20030219814A1
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; GENERAL INFORMATION:
; APPLICANT: Wan, David Chi-Cheong
; APPLICANT: Ip, Denis Tsz-Ming
; APPLICANT: The Chinese University of Hong Kong
; TITLE OF INVENTION: No. US20030219814A1e1 Fluorescent Proteins
; FILE REFERENCE: 016285-34-1
; CURRENT APPLICATION NUMBER: US/10/406,618
; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US 60/387,968
; PRIOR FILING DATE: 2002-06-11
; PRIOR APPLICATION NUMBER: US 60/370,598
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Spontaneously
; US-10-406-618-32

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QY 61 LSPQFQYGSKVYVKHPADIPDYKLSFPEGFKWERNMFEDGCVTVTTQDSSLQDGCFTY 120
DB 342 LSPQFQYGSKVYVKHPADIPDYKLSFPEGFKWERNMFEDGCVTVTTQDSSLQDGCFTY 401
QY 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFEFKSI 180
DB 402 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFEFKSI 461
QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIQEYERTEGRHHLFL 225
DB 462 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIQEYERTEGRHHLFL 506

RESULT 15

US-10-343-977-3
; Sequence 3, Application US/10343977
; Publication No. US20040014134A1
; GENERAL INFORMATION:
; APPLICANT: Kuhlemann, Rene
; APPLICANT: Koltermann, Andre
; APPLICANT: Ketting, Ulrich
; APPLICANT: Schwillle, Petra
; TITLE OF INVENTION: Dual coloured fluorimetric protease assay
; FILE REFERENCE: 023425us/JH/ml
; CURRENT APPLICATION NUMBER: US/10/343,977
; PRIOR APPLICATION NUMBER: 2003-02-06
; PRIOR FILING DATE: 2001-08-07
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 3
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Autofluorescent fusion protein derived from GFP variants of
; OTHER INFORMATION: e.g. Aequorea victoria and/or Discoma sp.
US-10-343-977-3

Query Match 100.0%; Score 1214; DB 15; Length 547;
Best Local Similarity 100.0%; Pred. No. 5.8e-120;
Matches 225; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 323 MRSSKNVIKEFMRFKVMEGTVNGHEFEIEGEGRPYEGHNTVKLKVTYKGGPLPFAWDI 382
QY 61 LSPQFQYGSKVYVKHPADIPDYKLSFPEGFKWERNMFEDGCVTVTTQDSSLQDGCFTY 120
DB 383 LSPQFQYGSKVYVKHPADIPDYKLSFPEGFKWERNMFEDGCVTVTTQDSSLQDGCFTY 442
QY 121 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFEFKSI 180
DB 443 KYKFIGVNFPSDGPVMQKTMGWEASTERLYPRDGLKGEIHKALKDKDGHYLVFEFKSI 502
QY 181 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIQEYERTEGRHHLFL 225
DB 503 YMAKKPVQLPGYVVYVDSKLDITSHNEDYTIQEYERTEGRHHLFL 547

Search completed: July 8, 2004, 10:00:33
Job time : 51 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 10:35:36 ; Search time 316 Seconds
(without alignments)
10457.256 Million cell updates/sec

Title: US-10-006-922A-11
Perfect score: 678
Sequence: 1 atgaggtcttccaagaatgt.....gccaccatctgtcctttaa 678

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3183909 seqs, 2436941669 residues
Total number of hits satisfying chosen parameters: 6367818

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	678	100.0	678	9	US-09-967-772-6 Sequence 6, Appli
2	678	100.0	678	13	US-10-132-067-3 Sequence 3, Appli
3	678	100.0	678	14	US-10-006-922-11 Sequence 11, Appli
4	678	100.0	678	15	US-10-121-258-2 Sequence 2, Appli
5	678	100.0	678	16	US-10-335-517-6 Sequence 6, Appli
6	678	100.0	678	16	US-10-334-288-6 Sequence 6, Appli
7	678	100.0	859	9	US-09-999-745-66 Sequence 66, Appli
8	678	100.0	859	10	US-09-866-538-11 Sequence 11, Appli
9	678	100.0	859	10	US-09-794-308-11 Sequence 11, Appli
10	678	100.0	859	10	US-09-865-291-11 Sequence 11, Appli
11	678	100.0	859	17	US-10-433-640-12 Sequence 12, Appli
12	677	99.9	3311	10	US-09-797-496B-3 Sequence 3, Appli
13	665	98.1	666	17	US-10-332-733-22 Sequence 22, Appli
14	661	97.5	711	17	US-10-314-936-1 Sequence 1, Appli

15	661	97.5	711	17	US-10-314-936-3	Sequence 3, Appli
16	658.8	97.2	898	14	US-10-006-922-45	Sequence 45, Appli
17	642.8	94.8	678	17	US-10-423-688A-40	Sequence 40, Appli
18	566.4	83.5	876	14	US-10-006-922-17	Sequence 17, Appli
19	566.4	83.5	876	15	US-10-161-403-39	Sequence 39, Appli
20	450.6	66.5	723	15	US-10-152-296-1	Sequence 1, Appli
21	450.6	66.5	723	17	US-10-739-656-1	Sequence 1, Appli
22	449.2	66.3	678	15	US-10-081-864-7	Sequence 7, Appli
23	449.2	66.3	678	15	US-10-315-920-1	Sequence 1, Appli
24	447.2	66.0	681	15	US-10-121-258-3	Sequence 3, Appli
25	447.2	66.0	681	15	US-10-121-258-23	Sequence 23, Appli
26	447.2	66.0	4692	15	US-10-161-403-29	Sequence 29, Appli
27	447.2	66.0	4692	17	US-10-433-640-16	Sequence 16, Appli
28	447.2	66.0	6984	14	US-10-001-189-45	Sequence 45, Appli
29	446	65.8	678	15	US-10-315-920-3	Sequence 3, Appli
30	445.8	65.8	1638	15	US-10-214-932-51	Sequence 51, Appli
31	445.8	65.8	1647	15	US-10-214-932-75	Sequence 75, Appli
32	445.6	65.7	681	14	US-10-006-922-35	Sequence 35, Appli
33	440.8	65.0	681	14	US-10-006-922-37	Sequence 37, Appli
34	439.6	64.8	678	15	US-10-315-920-5	Sequence 5, Appli
35	438	64.6	678	14	US-10-006-922-36	Sequence 36, Appli
36	438	64.6	678	15	US-10-081-864-14	Sequence 14, Appli
37	437	64.5	1050	14	US-10-060-857-7	Sequence 7, Appli
38	435.6	64.2	675	14	US-10-081-864-13	Sequence 38, Appli
39	435.6	64.2	675	15	US-10-081-864-13	Sequence 13, Appli
40	434.6	64.1	850	14	US-10-006-922-9	Sequence 9, Appli
41	432.2	63.7	678	15	US-10-121-258-5	Sequence 5, Appli
42	410.4	60.5	681	15	US-10-121-258-7	Sequence 7, Appli
43	409.6	60.4	699	9	US-09-967-772-5	Sequence 5, Appli
44	409.6	60.4	699	16	US-10-335-517-5	Sequence 5, Appli
45	409.6	60.4	699	16	US-10-334-288-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-967-772-6
; Sequence 6, Application US/09967772
; Patent No. US20020164577A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSUEN, Roger
; APPLICANT: GONZALEZ, Jesus
; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS
; FILE REFERENCE: REGEN1290.5
; CURRENT APPLICATION NUMBER: US/09/967,772
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: US 09/459,956
; PRIOR FILING DATE: 1999-12-13
; PRIOR APPLICATION NUMBER: US 08/765,860
; PRIOR FILING DATE: 1996-12-19
; PRIOR APPLICATION NUMBER: PCT/ US96/09652
; PRIOR FILING DATE: 1996-06-06
; PRIOR APPLICATION NUMBER: US 08/481,977
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp "red"
US-09-967-772-6

Query Match 100.0%; Score 678; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCTTCCAAGAATGTTATCAAGAGTTTCATGAGTTTAAGTTTCGATGAAGA 60
DB 1 ATGAGGTCTTCCAAGAATGTTATCAAGAGTTTCATGAGTTTAAGTTTCGATGAAGA 60
QY 61 ACGGTCAATGGGCAAGAGTTGAATAAGAGCGGAGGAGGAGCCATACGAAGC 120

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Db      61  ACGTCAATGGGCACGAGTTTGAATAGAAAGCGAAGAGAGGGAGGCCATACGAAGGC 120
QY      121  CACAATACCGTAAGCTTAAGTAAACCAAGGGGGACCTTTGCCATTTGCTGGATATT 180
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Db      121  CACAATACCGTAAGCTTAAGTAAACCAAGGGGGACCTTTGCCATTTGCTGGATATT 180
QY      181  TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAGCACCCCTGCCGACATACCA 240
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Db      181  TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAGCACCCCTGCCGACATACCA 240
QY      241  GACTATAAAAAGCTGTCAATTTCTGGAAGATTTAATGGGAAAGGTCATGAACCTTGAA 300
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Db      241  GACTATAAAAAGCTGTCAATTTCTGGAAGATTTAATGGGAAAGGTCATGAACCTTGAA 300
QY      301  GACGGTGGCGTCTGTACTGTAAACCCAGGATTCCAGTTTGACAGATGGCTGTTTCTAC 360
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Db      301  GACGGTGGCGTCTGTACTGTAAACCCAGGATTCCAGTTTGACAGATGGCTGTTTCTAC 360
QY      361  AAGGTCAAGTTCAATGGCGTGAACCTTTCCCTCCGATGACCTGTTATGCAAAAAGACACA 420
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Db      361  AAGGTCAAGTTCAATGGCGTGAACCTTTCCCTCCGATGACCTGTTATGCAAAAAGACACA 420
QY      421  ATGGGCTGGGAAGCCAGCACTGACGCTTTGTATCCTCGTATGGCGTGTGAAAGAGAG 480
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Db      421  ATGGGCTGGGAAGCCAGCACTGACGCTTTGTATCCTCGTATGGCGTGTGAAAGAGAG 480
QY      481  ATTCATAAGGCTCTGAAGCTGAAGAAGACGCGTGTCAATTAACCTAGTTGAATCAAAAGTATT 540
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Db      481  ATTCATAAGGCTCTGAAGCTGAAGAAGACGCGTGTCAATTAACCTAGTTGAATCAAAAGTATT 540
QY      541  TACATGGCAAGAAGCCCTGTGCAAGCTACCAAGGGTACTATATGTTGACTCCAACTGGAT 600
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Db      541  TACATGGCAAGAAGCCCTGTGCAAGCTACCAAGGGTACTATATGTTGACTCCAACTGGAT 600
QY      601  ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAACCAGGAGGACGC 660
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Db      601  ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAACCAGGAGGACGC 660
QY      661  CACCATCTGTTCTTTAA 678
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Db      661  CACCATCTGTTCTTTAA 678

RESULT 2
US-10-132-067-3
; Sequence 3, Application US/10132067
; Publication No. US20030203355A1
; GENERAL INFORMATION:
; APPLICANT: Bradbury, Andrew
; APPLICANT: Zeytun, Ahmet
; APPLICANT: Waldo, Geoffrey
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Fluorescence
; TITLE OF INVENTION: Binding Ligands With Intrinsic
; FILE REFERENCE: 021362-000600US
; CURRENT APPLICATION NUMBER: US/10/132, 067
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; OTHER INFORMATION: red fluorescent protein (dsRED)
; NAME/KEY: CDS
; LOCATION: (1)..(678)
; OTHER INFORMATION: dsRED
US-10-132-067-3
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Query Match 100.0%; Score 678; DB 13; Length 678;

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Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1  ATGAGTCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAAGTTCCGATGGAAGCA 60
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Db      1  ATGAGTCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAAGTTCCGATGGAAGCA 60
QY      61  ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGGAAGGAGGAGGCCATACGAAGGC 120
      |||||
Db      61  ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGGAAGGAGGAGGCCATACGAAGGC 120
QY      121  CACAATACCGTAAGCTTAAGTAAACCAAGGGGGACCTTTGCCATTTGCTGGATATT 180
      |||||
Db      121  CACAATACCGTAAGCTTAAGTAAACCAAGGGGGACCTTTGCCATTTGCTGGATATT 180
QY      181  TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAGCACCCCTGCCGACATACCA 240
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Db      241  GACTATAAAAAGCTGTCAATTTCTGGAAGATTTAATGGGAAAGGTCATGAACCTTGAA 300
QY      301  GACGGTGGCGTCTGTACTGTAAACCCAGGATTCCAGTTTGACAGATGGCTGTTTCTAC 360
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Db      301  GACGGTGGCGTCTGTACTGTAAACCCAGGATTCCAGTTTGACAGATGGCTGTTTCTAC 360
QY      361  AAGGTCAAGTTCAATGGCGTGAACCTTTCCCTCCGATGACCTGTTATGCAAAAAGACACA 420
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Db      361  AAGGTCAAGTTCAATGGCGTGAACCTTTCCCTCCGATGACCTGTTATGCAAAAAGACACA 420
QY      421  ATGGGCTGGGAAGCCAGCACTGACGCTTTGTATCCTCGTATGGCGTGTGAAAGAGAG 480
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Db      421  ATGGGCTGGGAAGCCAGCACTGACGCTTTGTATCCTCGTATGGCGTGTGAAAGAGAG 480
QY      481  ATTCATAAGGCTCTGAAGCTGAAGAAGACGCGTGTCAATTAACCTAGTTGAATCAAAAGTATT 540
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Db      481  ATTCATAAGGCTCTGAAGCTGAAGAAGACGCGTGTCAATTAACCTAGTTGAATCAAAAGTATT 540
QY      541  TACATGGCAAGAAGCCCTGTGCAAGCTACCAAGGGTACTATATGTTGACTCCAACTGGAT 600
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Db      541  TACATGGCAAGAAGCCCTGTGCAAGCTACCAAGGGTACTATATGTTGACTCCAACTGGAT 600
QY      601  ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAACCAGGAGGACGC 660
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Db      601  ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAACCAGGAGGACGC 660
QY      661  CACCATCTGTTCTTTAA 678
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Db      661  CACCATCTGTTCTTTAA 678
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RESULT 3
US-10-006-922-11
; Sequence 11, Application US/10006922
; Publication No. US20020197676A1
; GENERAL INFORMATION:
; APPLICANT: Lukyanov, Sergey A
; APPLICANT: Fradkov, Arcady F.
; APPLICANT: Labas, Yulii A.
; APPLICANT: Matz, Mikhail V.
; APPLICANT: Tersikh, Alexey
; TITLE OF INVENTION: No. US20020197676A1 Chromophores/Fluorophores and
; TITLE OF INVENTION: Methods for Using the Same
; FILE REFERENCE: CLON-035CIP
; CURRENT APPLICATION NUMBER: US/10/006, 922
; PRIOR APPLICATION NUMBER: 09/120, 330
; PRIOR FILING DATE: 1998-12-11
; PRIOR APPLICATION NUMBER: 09/457, 898
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/458, 144
; PRIOR FILING DATE: 1999-12-09
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; PRIOR APPLICATION NUMBER: 09/458,477
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/457,556
; PRIOR FILING DATE: 1999-12-09
; PRIOR APPLICATION NUMBER: 09/444,338
; PRIOR FILING DATE: 1999-11-19
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma species
US-10-006-922-11

Query Match 100.0%; Score 678; DB 14; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAGTTCCGATGGAAGA 60
DB 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAGTTCCGATGGAAGA 60
QY 61 ACCGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGCCATACGAAGGC 120
DB 61 ACCGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTGCTTGGATATT 180
DB 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTGCTTGGATATT 180
QY 181 TTGTACCAACAATTTCAAGTATGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA 240
DB 181 TTGTACCAACAATTTCAAGTATGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA 240
QY 241 GACTATAAAAGCTGTCAATTCCTGAAGATTTAATGGAAAGGTCATGAACCTTGAA 300
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DB 301 GACGGTGGCGTCTTACTGTAAACCCAGAGTTCCAGTTTGCAGGATGGCTTTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGAGCCTGTTATGCAAAAGAGACA 420
DB 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGAGCCTGTTATGCAAAAGAGACA 420
QY 421 ATGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGAGCGCTGTGAAGAGAG 480
DB 421 ATGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGAGCGCTGTGAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGCAAGTACCAAGGCTACTACTATGTGACTCCAACTGGAT 600
DB 541 TACATGGCAAGAAGCCTGTGCAAGTACCAAGGCTACTACTATGTGACTCCAACTGGAT 600
QY 601 ATAACAAGCCACAACGAAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
DB 601 ATAACAAGCCACAACGAAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

RESULT 4
US-10-121-258-2
; Sequence 2, Application US/10121258
; Publication No. US20030059835A1
; GENERAL INFORMATION:
; APPLICANT: Tsien, Roger

; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: MONOMERIC AND DIMERIC FLUORESCENT
; TITLE OF INVENTION: PROTEIN VARIANTS AND METHODS FOR MAKING SAME
; FILE REFERENCE: UC083.1CP2CP1
; CURRENT APPLICATION NUMBER: US/10/121,258
; CURRENT FILING DATE: 2002-04-10
; PRIOR APPLICATION NUMBER: 09/794,308
; PRIOR FILING DATE: 2001-02-26
; PRIOR APPLICATION NUMBER: 09/866,538
; PRIOR FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 678
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(678)
; OTHER INFORMATION: wild-type DsRed
US-10-121-258-2

Query Match 100.0%; Score 678; DB 15; Length 678;
Best Local Similarity 100.0%; Pred. No. 1.2e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAGTTCCGATGGAAGA 60
DB 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAGTTCCGATGGAAGA 60
QY 61 ACCGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGCCATACGAAGGC 120
DB 61 ACCGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTGCTTGGATATT 180
DB 121 CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGACCTTTGCCATTGCTTGGATATT 180
QY 181 TTGTACCAACAATTTCAAGTATGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA 240
DB 181 TTGTACCAACAATTTCAAGTATGAAGCAAGGTATATGTCAAGCAACCTGCGACATACCA 240
QY 241 GACTATAAAAGCTGTCAATTCCTGAAGATTTAATGGAAAGGTCATGAACCTTGAA 300
DB 241 GACTATAAAAGCTGTCAATTCCTGAAGATTTAATGGAAAGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAAACCCAGAGTTCCAGTTTGCAGGATGGCTTTTCATCTAC 360
DB 301 GACGGTGGCGTCTTACTGTAAACCCAGAGTTCCAGTTTGCAGGATGGCTTTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGAGCCTGTTATGCAAAAGAGACA 420
DB 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGAGCCTGTTATGCAAAAGAGACA 420
QY 421 ATGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGAGCGCTGTGAAGAGAG 480
DB 421 ATGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGAGCGCTGTGAAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAGGCTCTGAAGCTGAAGAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGCAAGTACCAAGGCTACTACTATGTGACTCCAACTGGAT 600
DB 541 TACATGGCAAGAAGCCTGTGCAAGTACCAAGGCTACTACTATGTGACTCCAACTGGAT 600
QY 601 ATAACAAGCCACAACGAAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
DB 601 ATAACAAGCCACAACGAAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
QY 661 CACCATCTGTTCTTTAA 678
DB 661 CACCATCTGTTCTTTAA 678

RESULT 5

US-10-335-517-6

; Sequence 6, Application US/10335517
; Publication No. US20030207248A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: TSIEH, Roger

; APPLICANT: GONZALEZ, Jesus

; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS

; FILE REFERENCE: REGEN1290-5

; CURRENT FILING DATE: US/10/335,517

; PRIOR FILING DATE: 2002-12-31

; PRIOR FILING DATE: US/09/967,772

; PRIOR FILING DATE: 2001-09-28

; PRIOR FILING DATE: US 09/459,956

; PRIOR FILING DATE: 1999-12-13

; PRIOR FILING DATE: US 08/765,860

; PRIOR FILING DATE: 1996-12-19

; PRIOR APPLICATION NUMBER: PCT/ US96/09652

; PRIOR FILING DATE: 1996-06-06

; PRIOR APPLICATION NUMBER: US 08/481,977

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 678

; TYPE: DNA

; ORGANISM: Discosoma sp "red"

US-10-335-517-6

Query Match 100.0%; Score 678; DB 16; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.2e-218; Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGTCTTCCAGAAATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
    |||
Db 1 ATGAGTCTTCCAGAAATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
QY 61 ACGTCAATGGGCACGAGTTTGAATAGAGCGCAAGAGGGGAGGCCATACGAAGGC 120
    |||
Db 61 ACGTCAATGGGCACGAGTTTGAATAGAGCGCAAGAGGGGAGGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTCCATTTGCTGGGATATT 180
    |||
Db 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTCCATTTGCTGGGATATT 180
QY 181 TTGTCAACCAATTTCAATATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
    |||
Db 181 TTGTCAACCAATTTCAATATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
QY 241 GACTATAAAAAAGCTGTCAATTTCTGGAAGATTTAAATGGAAAGGTCATGAACCTTGAA 300
    |||
Db 241 GACTATAAAAAAGCTGTCAATTTCTGGAAGATTTAAATGGAAAGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAACCCAGGATTTCCAGTTTGACAGATGGCTGTTTCATCTAC 360
    |||
Db 301 GACGGTGGCGTCTTACTGTAACCCAGGATTTCCAGTTTGACAGATGGCTGTTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGACA 420
    |||
Db 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGTGTGTAAGAGAGAG 480
    |||
Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGCGTGTGTAAGAGAGAG 480
QY 481 ATTCAATAGGCTCTGAAGCTGAAGAAGCGGTGTCAATTAAGTTGAATTCAAAAGTATT 540
    |||
Db 481 ATTCAATAGGCTCTGAAGCTGAAGAAGCGGTGTCAATTAAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCGTGTGCAAGCTACCAAGGTAATACTATGTGACTCCAACCTGGAT 600
```

```
Db 541 TACATGGCAAGAAGCCGTGTGCAAGCTACCAAGGTAATACTATGTGACTCCAACCTGGAT 600
QY 601 ATAACAAGCCACAACGAGACTATACATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660
    |||
Db 601 ATAACAAGCCACAACGAGACTATACATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
    |||
Db 661 CACCATCTGTTCTTTAA 678
```

RESULT 6

US-10-334-288-6

; Sequence 6, Application US/10334288

; Publication No. US20040002123A1

; GENERAL INFORMATION:

; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA

; APPLICANT: TSIEH, Roger

; APPLICANT: GONZALEZ, Jesus

; TITLE OF INVENTION: DETECTION OF TRANSMEMBRANE POTENTIALS BY OPTICAL METHODS

; FILE REFERENCE: REGEN1290-5

; CURRENT FILING DATE: US/10/334,288

; PRIOR FILING DATE: 2002-12-31

; PRIOR FILING DATE: US/09/967,772

; PRIOR FILING DATE: 2001-09-28

; PRIOR FILING DATE: US 09/459,956

; PRIOR FILING DATE: 1999-12-13

; PRIOR FILING DATE: US 08/765,860

; PRIOR FILING DATE: 1996-12-19

; PRIOR APPLICATION NUMBER: PCT/ US96/09652

; PRIOR FILING DATE: 1996-06-06

; PRIOR APPLICATION NUMBER: US 08/481,977

; PRIOR FILING DATE: 1995-06-07

; NUMBER OF SEQ ID NOS: 22

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 6

; LENGTH: 678

; TYPE: DNA

; ORGANISM: Discosoma sp "red"

US-10-334-288-6

Query Match 100.0%; Score 678; DB 16; Length 678;

Best Local Similarity 100.0%; Pred. No. 1.2e-218; Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGTCTTCCAGAAATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
    |||
Db 1 ATGAGTCTTCCAGAAATGTTATCAAGAGTTCATGAGTTTAAGTTTCGATGGAAGA 60
QY 61 ACGTCAATGGGCACGAGTTTGAATAGAGCGCAAGAGGGGAGGCCATACGAAGGC 120
    |||
Db 61 ACGTCAATGGGCACGAGTTTGAATAGAGCGCAAGAGGGGAGGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTCCATTTGCTGGGATATT 180
    |||
Db 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTCCATTTGCTGGGATATT 180
QY 181 TTGTCAACCAATTTCAATATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
    |||
Db 181 TTGTCAACCAATTTCAATATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
QY 241 GACTATAAAAAAGCTGTCAATTTCTGGAAGATTTAAATGGGAAGGTCATGAACCTTGAA 300
    |||
Db 241 GACTATAAAAAAGCTGTCAATTTCTGGAAGATTTAAATGGGAAGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAACCCAGGATTTCCAGTTTGACAGATGGCTGTTTCATCTAC 360
    |||
Db 301 GACGGTGGCGTCTTACTGTAACCCAGGATTTCCAGTTTGACAGATGGCTGTTTCATCTAC 360
QY 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGACA 420
    |||
Db 361 AAGGTCAAGTTCATTTGGCGTGAACCTTCTCCGATGGAACCTGTATGCAAAAGAGACA 420
```

```
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCTCGTGATGGCGTGTGAAAGGAGAG 480
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCTCGTGATGGCGTGTGAAAGGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGACCTGTGACAGCTACCAAGGCTACTACTATGTTGACTCCAAACTGAT 600
DB 541 TACATGGCAAGAAGACCTGTGACAGCTACCAAGGCTACTACTATGTTGACTCCAAACTGAT 600
QY 601 ATACAAGCCACAAGCAAGAGACTATACATCGTTGAGCAGTATGAAAGAACCGAGGAGCGC 660
DB 601 ATACAAGCCACAAGCAAGAGACTATACATCGTTGAGCAGTATGAAAGAACCGAGGAGCGC 660
QY 661 CACCATCTGTCTCTTAA 678
DB 661 CACCATCTGTCTCTTAA 678
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RESULT 7

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US-09-999-745-66
; Sequence 66, Application US/09999745
; Patent No. US20020157120A1
; GENERAL INFORMATION:
; APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: Tsien, Roger Y.
; APPLICANT: Baird, Geoffrey
; TITLE OF INVENTION: CIRCULARLY PERMUTED FLUORESCENT PROTEIN INDICATORS
; FILE REFERENCE: REGEN1470-1
; CURRENT APPLICATION NUMBER: US/09/999,745
; CURRENT FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: 09/316,920
; PRIOR FILING DATE: 1999-05-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 66
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
; US-09-999-745-66
```

Query Match

Best local Similarity 100.0%; Score 678; DB 9; Length 859;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ATGAGGCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAGTTTCGCATGGAAGA 60
DB 54 ATGAGGCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAGTTTCGCATGGAAGA 113
QY 61 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGAGGAGGCCATACGAAGGC 120
DB 114 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTGGCATTTGCTGGGATATT 180
DB 174 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTGGCATTTGCTGGGATATT 233
QY 181 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCGCATACCA 240
DB 234 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCGCATACCA 293
QY 241 GACTATAAAAAGCTGTCATTTCTGAAGGATTTAAATGGAAAAGGTCATGAACCTTGA 300
DB 294 GACTATAAAAAGCTGTCATTTCTGAAGGATTTAAATGGAAAAGGTCATGAACCTTGA 353
QY 301 GACGGTGGCGTCTGTAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
```

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DB 354 GACGGTGGCGTCTGTAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 413
QY 361 AAGGTCAAGTTTCAATTTGGCGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAAGAGACA 420
DB 414 AAGGTCAAGTTTCAATTTGGCGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCTCGTGATGGCGTGTGAAAGGAGAG 480
DB 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCTCGTGATGGCGTGTGAAAGGAGAG 533
QY 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTACCTAGTTGAATTCAAAAGTATT 540
DB 534 ATTCAATAAGGCTCTGAAGCTGAAAGACGGTGTCAATTACCTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAGAAGACCTGTGACAGCTACCAAGGCTACTACTATGTTGACTCCAAACTGAT 600
DB 594 TACATGGCAAGAAGACCTGTGACAGCTACCAAGGCTACTACTATGTTGACTCCAAACTGAT 653
QY 601 ATACAAGCCACAAGCAAGAGACTATACATCGTTGAGCAGTATGAAAGAACCGAGGAGCGC 660
DB 654 ATACAAGCCACAAGCAAGAGACTATACATCGTTGAGCAGTATGAAAGAACCGAGGAGCGC 713
QY 661 CACCATCTGTCTCTTAA 678
DB 714 CACCATCTGTCTCTTAA 731
```

RESULT 8

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US-09-866-538-11
; Sequence 11, Application US/09866538
; Publication No. US20030032088A1
; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSIENT, Robert
; APPLICANT: Campbell, Robert
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530-2
; CURRENT APPLICATION NUMBER: US/09/866,538
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)..(731)
; US-09-866-538-11
```

Query Match

Best local Similarity 100.0%; Score 678; DB 10; Length 859;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGGCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAGTTTCGCATGGAAGA 60
DB 54 ATGAGGCTTCCAGAATGTTATCAAGGATTCATGAGGTTTAAGTTTCGCATGGAAGA 113
QY 61 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGAGGAGGCCATACGAAGGC 120
DB 114 ACGTCAATGGGCAAGATTGAAATAGAAAGCGAAGAGAGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTGGCATTTGCTGGGATATT 180
DB 174 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGACCTTGGCATTTGCTGGGATATT 233
QY 181 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCGCATACCA 240
DB 234 TTGTCAACCAATTTCAAGTATGGAAGCAAGGTAATGTCAAGCAACCTGCGCATACCA 293
QY 241 GACTATAAAAAGCTGTCATTTCTGAAGGATTTAAATGGAAAAGGTCATGAACCTTGA 300
DB 294 GACTATAAAAAGCTGTCATTTCTGAAGGATTTAAATGGAAAAGGTCATGAACCTTGA 353
```



```
QY 301 GACGGTGGCGTCGTTACTGTAACCCAGGATTCAGTTGCGAGGATGGCTGTTTCATCTAC 360
    |||||||
Db 354 GACGGTGGCGTCGTTACTGTAACCCAGGATTCAGTTGCGAGGATGGCTGTTTCATCTAC 413

QY 361 AAGGTCAAGTTCATGGCGGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAGAAGACA 420
    |||||||
Db 414 AAGGTCAAGTTCATGGCGGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAGAAGACA 473

QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAGAGAG 480
    |||||||
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAGAGAG 533

QY 481 ATTCATAAGGCTCTGAAGCTGAAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAGTATT 540
    |||||||
Db 534 ATTCATAAGGCTCTGAAGCTGAAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAGTATT 593

QY 541 TACATGGCAAGAAGCCTGTGCAGCTACCGAGGTACTACTATGTGACTCCAAACTGGAT 600
    |||||||
Db 594 TACATGGCAAGAAGCCTGTGCAGCTACCGAGGTACTACTATGTGACTCCAAACTGGAT 653

QY 601 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 660
    |||||||
Db 654 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 713

QY 661 CACCATCTGTTCCCTTAA 678
    |||||||
Db 714 CACCATCTGTTCCCTTAA 731
```

RESULT 9
US-09-794-308-11
; Sequence 11, Application US/09794308
; Publication No. US20030170911A1

; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: ZACHARIAS, David
; APPLICANT: BAIRD, Geoffrey
; TITLE OF INVENTION: NON-OLIGOMERIZING FLUORESCENT PROTEINS
; FILE REFERENCE: REGEN1530
; CURRENT APPLICATION NUMBER: US/09/794,308
; CURRENT FILING DATE: 2001-02-26
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54) .. (731)
US-09-794-308-11

Query Match 100.0%; Score 678; DB 10; Length 859;
Best Local Similarity 100.0%; Pred. No. 1.4e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGTCTTCCAAGATGTTATCAAGAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGA 60
    |||||||
Db 54 ATGAGTCTTCCAAGATGTTATCAAGAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGA 113

QY 61 ACGGTCAATGGGACGAGATTGAAATAGAGGCGAAGAGAGAGGGGAGGCCATACGAAGGC 120
    |||||||
Db 114 ACGGTCAATGGGACGAGATTGAAATAGAGGCGAAGAGAGAGGGGAGGCCATACGAAGGC 173

QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTGGGATATT 180
    |||||||
Db 174 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTGGGATATT 233

QY 181 TTGTCAACCACAATTCAGTATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
    |||||||
Db 234 TTGTCAACCACAATTCAGTATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 293
```

```
QY 241 GACTATATAAAAGCTGTCAATTCCTGGAAGGATTTAAATGGGAAAGGTCATGAACCTTGAA 300
    |||||||
Db 294 GACTATATAAAAGCTGTCAATTCCTGGAAGGATTTAAATGGGAAAGGTCATGAACCTTGAA 353

QY 301 GACGTGGCGTCGTTACTGTAACCCAGGATTCAGTTGCGAGGATGGCTGTTTCATCTAC 360
    |||||||
Db 354 GACGTGGCGTCGTTACTGTAACCCAGGATTCAGTTGCGAGGATGGCTGTTTCATCTAC 413

QY 361 AAGGTCAAGTTCATGGCGGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAGAAGACA 420
    |||||||
Db 414 AAGGTCAAGTTCATGGCGGTGAACCTTCCCTCCGATGGACCTGTTATGCAAAAGAAGACA 473

QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAGAGAG 480
    |||||||
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTGATGGCGTGTGAAGAGAG 533

QY 481 ATTCATAAGGCTCTGAAGCTGAAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAGTATT 540
    |||||||
Db 534 ATTCATAAGGCTCTGAAGCTGAAAAGACGGTGTCAATTAACCTAGTTGAATTCAAAAGTATT 593

QY 541 TACATGGCAAGAAGCCTGTGCAGCTACCGAGGTACTACTATGTGACTCCAAACTGGAT 600
    |||||||
Db 594 TACATGGCAAGAAGCCTGTGCAGCTACCGAGGTACTACTATGTGACTCCAAACTGGAT 653

QY 601 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 660
    |||||||
Db 654 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 713

QY 661 CACCATCTGTTCCCTTAA 678
    |||||||
Db 714 CACCATCTGTTCCCTTAA 731
```

RESULT 10
US-09-865-291-11
; Sequence 11, Application US/09865291
; Publication No. US20030186229A1

; GENERAL INFORMATION:
; APPLICANT: REGENTS OF THE UNIVERSITY OF CALIFORNIA
; APPLICANT: TSJEN, Roger
; APPLICANT: TING, Alice
; APPLICANT: ZHANG, Jin
; TITLE OF INVENTION: EMISSION RATIONETRIC INDICATORS OF PHOSPHORYLATION
; FILE REFERENCE: REGEN1550
; CURRENT APPLICATION NUMBER: US/09/865,291
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54) .. (731)
US-09-865-291-11

Query Match 100.0%; Score 678; DB 10; Length 859;
Best Local Similarity 100.0%; Pred. No. 1.4e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 ATGAGTCTTCCAAGATGTTATCAAGAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGA 60
    |||||||
Db 54 ATGAGTCTTCCAAGATGTTATCAAGAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGA 113

QY 61 ACGGTCAATGGGACGAGATTGAAATAGAGGCGAAGGAGAGGGGAGGCCATACGAAGGC 120
    |||||||
Db 114 ACGGTCAATGGGACGAGATTGAAATAGAGGCGAAGGAGAGGGGAGGCCATACGAAGGC 173

QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGAGCCTTTGCCATTGCTGGGATATT 180
    |||||||
Db 174 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGAGCCTTTGCCATTGCTGGGATATT 233
```



```

QY 181 TTGTACCACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
    |||||||
Db 234 TTGTACCACAAAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 293
QY 241 GACTATAAAAAGCTGTCTATTCTCGAAGATTTAAATGGAAAGGTCATGAACTTTGAA 300
    |||||||
Db 294 GACTATAAAAAGCTGTCTATTCTCGAAGATTTAAATGGAAAGGTCATGAACTTTGAA 353
QY 301 GACGGTGGCGTCTGTTACTGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
    |||||||
Db 354 GACGGTGGCGTCTGTTACTGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 413
QY 361 AAGGTCAAGTTCAATTGGCGTGAACCTTCCGATGGACCTGTATGCAAAAGAGACA 420
    |||||||
Db 414 AAGGTCAAGTTCAATTGGCGTGAACCTTCCGATGGACCTGTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTAAGAGAGAG 480
    |||||||
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTAAGAGAGAG 533
QY 481 ATTCAATAAGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
    |||||||
Db 534 ATTCAATAAGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCCCTGTGACGCTACCAAGGTACTACTATGTGACTCCAACTGAT 600
    |||||||
Db 594 TACATGGCAAGAAGCCCTGTGACGCTACCAAGGTACTACTATGTGACTCCAACTGAT 653
QY 601 ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGC 660
    |||||||
Db 654 ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGC 713
QY 661 CACCATCTGTTCTTTAA 678
    |||||||
Db 714 CACCATCTGTTCTTTAA 731

```

RESULT 11

```

US-10-433-640-12
; Sequence 12, Application US/10433640
; Publication No. US20040115792A1
; GENERAL INFORMATION:
; APPLICANT: Lichtenberg-Frate, Hella
; TITLE OF INVENTION: YEAST STRAIN FOR TESTING THE GENOTOXICITY AND CYTOTOXICITY OF
; TITLE OF INVENTION: COMPLEX ENVIRONMENTAL CONTAMINATIONS
; FILE REFERENCE: 1487/3
; CURRENT APPLICATION NUMBER: US/10/433, 640
; CURRENT FILING DATE: 2003-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/14610
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: DE 10061872.3
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 859
; TYPE: DNA
; ORGANISM: Discosoma sp.
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54) ..(731)
; US-10-433-640-12

```

```

Query Match 100.0%; Score 678; DB 17; Length 859;
Best Local Similarity 100.0%; Pred. No. 1.4e-218;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTTCGATGGAAGA 60
    |||||||
Db 54 ATGAGGTCTTCCAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTTCGATGGAAGA 113
QY 61 ACGGTCAATGGGACGAGTTTGAATAAGGAAGGAGAGAGGGGACCATACGAAGGC 120

```

```

Db 114 ACGGTCAATGGGACGAGTTTGAATAAGGAAGGCGAAGGAGAGGGGACCATACGAAGGC 173
QY 121 CACAATAACCGTAAGCTTTAAGGTAACCAAGGGGGACCTTTGCCATTTGCTGGGATATT 180
    |||||||
Db 174 CACAATAACCGTAAGCTTTAAGGTAACCAAGGGGGACCTTTGCCATTTGCTGGGATATT 233
QY 181 TTGTACCACAATTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
    |||||||
Db 234 TTGTACCACAATTTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 293
QY 241 GACTATAAAAAGCTGTCTATTCTCGAAGATTTAAATGGGAAGGTCATGAACTTTGAA 300
    |||||||
Db 294 GACTATAAAAAGCTGTCTATTCTCGAAGATTTAAATGGGAAGGTCATGAACTTTGAA 353
QY 301 GACGGTGGCGTCTGTTACTGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
    |||||||
Db 354 GACGGTGGCGTCTGTTACTGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 413
QY 361 AAGGTCAAGTTCAATTGGCGTGAACCTTCCGATGGACCTGTATGCAAAAGAGACA 420
    |||||||
Db 414 AAGGTCAAGTTCAATTGGCGTGAACCTTCCGATGGACCTGTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTAAGAGAGAG 480
    |||||||
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCTCGTATGGCGGTGTAAGAGAGAG 533
QY 481 ATTCAATAAGCTCTGAAGCTGAAAGAAGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
    |||||||
Db 534 ATTCAATAAGCTCTGAAGCTGAAAGAAGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCCCTGTGACGCTACCAAGGTACTACTATGTGACTCCAACTGAT 600
    |||||||
Db 594 TACATGGCAAGAAGCCCTGTGACGCTACCAAGGTACTACTATGTGACTCCAACTGAT 653
QY 601 ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGC 660
    |||||||
Db 654 ATAACAAGCCACAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGACGC 713
QY 661 CACCATCTGTTCTTTAA 678
    |||||||
Db 714 CACCATCTGTTCTTTAA 731

```

RESULT 12

```

US-09-797-496B-3
; Sequence 3, Application US/09797496B
; Publication No. US20030049597A1
; GENERAL INFORMATION:
; APPLICANT: Simon, Sanford M.
; TITLE OF INVENTION: Chimeric Fluorescent Enzymes and Uses Thereof
; FILE REFERENCE: 600-1-267
; CURRENT APPLICATION NUMBER: US/09/797, 496B
; CURRENT FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 3311
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Discosoma red fluorescent protein modified as described in specif
; OTHER INFORMATION: ication.
; US-09-797-496B-3

```

```

Query Match 99.9%; Score 677; DB 10; Length 3311;
Best Local Similarity 100.0%; Pred. No. 6.9e-218;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGTCTTCCAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTTCGATGGAAGA 60
    |||||||
Db 289 ATGAGGTCTTCCAAGATGTTATCAAGAGTTCATGAGTTTAAGTTTTCGATGGAAGA 348

```

```
QY      61  ACGTCAATGGGCACGACGTTTGAATAGAAAGGCGAAGAGAGAGGGGAGGCCATACGAAGGC 120
      |||
Db      349  ACGTCAATGGGCACGACGTTTGAATAGAAAGGCGAAGAGAGAGGGGAGGCCATACGAAGGC 408
QY      121  CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGTGCGGATATT 180
      |||
Db      409  CACAATACCGTAAAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGTGCGGATATT 468
QY      181  TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATGTCAAGCACCCCTGCCGACATACCA 240
      |||
Db      469  TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATGTCAAGCACCCCTGCCGACATACCA 528
QY      241  GACTATAAAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAAGGTCATGAATTGAA 300
      |||
Db      529  GACTATAAAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAAGGTCATGAATTGAA 588
QY      301  GACGGTGGCGTCTTACTGTAAACCCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
      |||
Db      589  GACGGTGGCGTCTTACTGTAAACCCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 648
QY      361  AAGTCAAGTTCAATGGCGGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAACA 420
      |||
Db      649  AAGTCAAGTTCAATGGCGGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAACA 708
QY      421  ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTGATGGCGTGTGAAGAGAG 480
      |||
Db      709  ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTGATGGCGTGTGAAGAGAG 768
QY      481  ATTCAATAAGGCTCTGAAGCTGAAGAAGACGGTGTCAATTAAGTTGAATTCAAAAGTATT 540
      |||
Db      769  ATTCAATAAGGCTCTGAAGCTGAAGAAGACGGTGTCAATTAAGTTGAATTCAAAAGTATT 828
QY      541  TACATGGCAAGAAGCCCTGTGACAGCTACCAAGGTACTATGTGACTCCAAACTGGAT 600
      |||
Db      829  TACATGGCAAGAAGCCCTGTGACAGCTACCAAGGTACTATGTGACTCCAAACTGGAT 888
QY      601  ATAAACAAGCCACAACGAACTATACAATCGTTGAGCAGATGAAAGAACCAGAGGAGCGC 660
      |||
Db      889  ATAAACAAGCCACAACGAACTATACAATCGTTGAGCAGATGAAAGAACCAGAGGAGCGC 948
QY      661  CACCATCTGTTCTTTA 677
      |||
Db      949  CACCATCTGTTCTTTA 965
```

```
RESULT 13
US-10-332-733-22
; Sequence 22, Application US/10332733
; Publication No. US20040106565A1
; GENERAL INFORMATION:
; APPLICANT: Margarete Odenthal and Diana Jung
; TITLE OF INVENTION: Gene Expression, Genome Alteration And Reporter Expression
; FILE REFERENCE: 1472/68806
; CURRENT APPLICATION NUMBER: US/10/332,733
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; LENGTH: 666
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence: Red
US-10-332-733-22
```

```
Query Match      98.1%; Score 665; DB 17; Length 666;
Best Local Similarity 100.0%; Pred. No. 3.1e-214;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 13 AAGAATGTATCAAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGAACGTCATATGGG 72

```
Db      1  AAGAATGTATCAAGAGTTCATGAGGTTTAAGGTTCCGATGGAAGAACGTCATATGGG 60
      |||
QY      73  CACGAGTTTGAATAGAAAGGCGAAGAGAGAGGGAGGCCATACGAAGGCCACAATACCGTA 132
      |||
Db      61  CACGAGTTTGAATAGAAAGGCGAAGAGAGAGGGAGGCCATACGAAGGCCACAATACCGTA 120
QY      133  AAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGTGCGGATATTGTCACACCAA 192
      |||
Db      121  AAGCTTAAGGTAAACCAAGGGGGGACCTTTGCCATTGTGCGGATATTGTCACACCAA 180
QY      193  TTTCAGTATGGAAGCAAGGATATATGTCAAGCACCCCTGCCGACATACCACTATAAAAAAG 252
      |||
Db      181  TTTCAGTATGGAAGCAAGGATATATGTCAAGCACCCCTGCCGACATACCACTATAAAAAAG 240
QY      253  CTGTCAATTTCTGGAAGGATTTAAATGGGAAAAGGTCATGAACCTTGAAGACGGTGGCGTC 312
      |||
Db      241  CTGTCAATTTCTGGAAGGATTTAAATGGGAAAAGGTCATGAACCTTGAAGACGGTGGCGTC 300
QY      313  GTTACTGTAAACCCAGGATTCAGTTTGACAGGATGGCTGTTTCATCTACAAAGTCAAGTTC 372
      |||
Db      301  GTTACTGTAAACCCAGGATTCAGTTTGACAGGATGGCTGTTTCATCTACAAAGTCAAGTTC 360
QY      373  ATTGCGGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAACAATGGGCTGGGAA 432
      |||
Db      361  ATTGCGGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAACAATGGGCTGGGAA 420
QY      433  GCCAGCACTGAGCGTTTGATCCTCGTGATGGCGTGTGAAGAGAGAGATTCAATAGGCT 492
      |||
Db      421  GCCAGCACTGAGCGTTTGATCCTCGTGATGGCGTGTGAAGAGAGAGATTCAATAGGCT 480
QY      493  CTGAAGCTGAAGAAGACGGTGTCAATTAAGTTGAATTCAAAAGTATTACATGSCAAAG 552
      |||
Db      481  CTGAAGCTGAAGAAGACGGTGTCAATTAAGTTGAATTCAAAAGTATTACATGSCAAAG 540
QY      553  AAGCCTGTGAGCTACCAAGGTACTACTATGTGACTCCAAACTGGAATATAACAAGCCAC 612
      |||
Db      541  AAGCCTGTGAGCTACCAAGGTACTACTATGTGACTCCAAACTGGAATATAACAAGCCAC 600
QY      613  AAGGAAGACTATACAATCGTTGAGCAGATGAAAGAACCAGAGGAGCCACCATCTGTTTC 672
      |||
Db      601  AAGGAAGACTATACAATCGTTGAGCAGATGAAAGAACCAGAGGAGCCACCATCTGTTTC 660
QY      673  CTTTA 677
      |||
Db      661  CTTTA 665
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RESULT 14
US-10-314-936-1
; Sequence 1, Application US/10314936
; Publication No. US20040110225A1
; GENERAL INFORMATION:
; APPLICANT: Gibbs, Patrick D.L.
; APPLICANT: Carter, Robert W.
; TITLE OF INVENTION: SCHMALE, MICHAEL C.
; FILE REFERENCE: 638.004
; CURRENT APPLICATION NUMBER: US/10/314,936
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: mutant red fluorescent protein
; NAME/KEY: CDS
; LOCATION: (1)..(711)
; OTHER INFORMATION:
US-10-314-936-1
```

Query Match 97.5%; Score 661; DB 17; Length 711;
 Best Local Similarity 98.5%; Pred. No. 7.2e-213;
 Matches 667; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 ATGAGTCTTCCAAGAATGTTATCAAGAGTTCATGAGGTTTAAGTTTCGATGGAAGA 60
    |||||
DB 1 ATGAGTGTTCGAAGAATGTTATCAAGAGTTCATGAGGTTTAAGTTTCGATGGAAGA 60
QY 61 ACGTCAATGGGCAAGAGTTTGAATAGAAGCGAAGAGAGAGGGGAGGCCATACGAAGC 120
    |||||
DB 61 ACGTCAATGGGCAAGAGTTTGAATAGAAGCGAAGAGAGAGGGGAGGCCATACGAAGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTGGCCATTGGCTGGATATT 180
    |||||
DB 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTGGCCATTGGCTGGATATT 180
QY 181 TTGTACACCAATTTCAAGTATGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
    |||||
DB 181 TTGTACACCAATTTCAAGTATGAAGCAAGGTATATGTCAAGCATCTGCGACATACCA 240
QY 241 GACTATAAAGCTGTCTATTTCTGAAGAGTTTAATGGAAAGGTCATGAACCTTGAA 300
    |||||
DB 241 GACTATAAAGCTGTCTATTTCTGAAGAGTTTAATGGAAAGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTACTGTAAACCCAGATTTCCAGTTTGACAGATGGCTTTCATCTAC 360
    |||||
DB 301 GACGGTGGCGTCTACTGTAAACCCAGATTTCCAGTTTGACAGATGGCTTTCATCTAC 360
QY 361 AAGTCAAGTTCAATTGGCGTGAACCTTCCGATGGAACCTGTATGCAAAAGAGACA 420
    |||||
DB 361 AAGTCAAGTTCAATTGGCGTGAACCTTCCGATGGAACCTGTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTAAGAGAGAG 480
    |||||
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTAAGAGAGAG 480
QY 481 ATTCAATAAGGCTTGAAGCTGAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
    |||||
DB 481 ATTCAATAAGGCTTGAAGCTGAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGACGTACAGGGTACTACTATGTGACTCCAACTGGAT 600
    |||||
DB 541 TACATGGCAAGAAGCCTGTGACGTACAGGGTACTACTATGTGACTCCAACTGGAT 600
QY 601 ATAACAAGCCACAAGAGACTATCAATCGTTGAGCAGTATGAAGAACCAGAGGAGCG 660
    |||||
DB 601 ATAACAAGCCACAAGAGACTATCAATCGTTGAGCAGTATGAAGAACCAGAGGAGCG 660
QY 661 CACCATCTGTTCCTTTA 677
    |||||
DB 661 CACCATCTGTTCCTTTA 677
    |||||

```

RESULT 15

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US-10-314-936-3
; Sequence 3, Application US/10314936
; Publication No. US20040110225A1
; GENERAL INFORMATION:
; APPLICANT: Gibbs, Patrick D.L.
; APPLICANT: Carter, Robert W.
; APPLICANT: Schmale, Michael C.
; TITLE OF INVENTION: FLUORESCENT PROTEINS FROM AQUATIC SPECIES
; FILE REFERENCE: 638.004
; CURRENT APPLICATION NUMBER: US/10/314,936
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:

```

OTHER INFORMATION: mutant red fluorescent protein
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(711)
 ; OTHER INFORMATION:
 ; US-10-314-936-3

Query Match 97.5%; Score 661; DB 17; Length 711;
 Best Local Similarity 98.5%; Pred. No. 7.2e-213;
 Matches 667; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

```

QY 1 ATGAGTCTTCCAAGAATGTTATCAAGAGTTCATGAGGTTTAAGTTTCGATGGAAGA 60
    |||||
DB 1 ATGAGTGTTCGAAGAATGTTATCAAGAGTTCATGAGGTTTAAGTTTCGATGGAAGA 60
QY 61 ACGTCAATGGGCAAGAGTTTGAATAGAAGCGAAGAGAGAGGGGAGGCCATACGAAGC 120
    |||||
DB 61 ACGTCAATGGGCAAGAGTTTGAATAGAAGCGAAGAGAGAGGGGAGGCCATACGAAGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTGGCCATTGGCTGGATATT 180
    |||||
DB 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTGGCCATTGGCTGGATATT 180
QY 181 TTGTACACCAATTTCAAGTATGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
    |||||
DB 181 TTGTACACCAATTTCAAGTATGAAGCAAGGTATATGTCAAGCATCTGCGACATACCA 240
QY 241 GACTATAAAGCTGTCTATTTCTGAAGAGTTTAATGGGAAGGTCATGAACCTTGAA 300
    |||||
DB 241 GACTATAAAGCTGTCTATTTCTGAAGAGTTTAATGGGAAGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTACTGTAAACCCAGATTTCCAGTTTGACAGATGGCTTTCATCTAC 360
    |||||
DB 301 GACGGTGGCGTCTACTGTAAACCCAGATTTCCAGTTTGACAGATGGCTTTCATCTAC 360
QY 361 AAGTCAAGTTCAATTGGCGTGAACCTTCCGATGGAACCTGTATGCAAAAGAGACA 420
    |||||
DB 361 AAGTCAAGTTCAATTGGCGTGAACCTTCCGATGGAACCTGTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTAAGAGAGAG 480
    |||||
DB 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGGTGTAAGAGAGAG 480
QY 481 ATTCAATAAGGCTTGAAGCTGAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
    |||||
DB 481 ATTCAATAAGGCTTGAAGCTGAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGACGTACAGGGTACTACTATGTGACTCCAACTGGAT 600
    |||||
DB 541 TACATGGCAAGAAGCCTGTGACGTACAGGGTACTACTATGTGACTCCAACTGGAT 600
QY 601 ATAACAAGCCACAAGAGACTATCAATCGTTGAGCAGTATGAAGAACCAGAGGAGCG 660
    |||||
DB 601 ATAACAAGCCACAAGAGACTATCAATCGTTGAGCAGTATGAAGAACCAGAGGAGCG 660
QY 661 CACCATCTGTTCCTTTA 677
    |||||
DB 661 CACCATCTGTTCCTTTA 677
    |||||

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Search completed: July 11, 2004, 12:17:49
 Job time : 318 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: July 11, 2004, 08:19:25 ; Search time 305 Seconds
(without alignments)
9443.535 Million cell updates/sec

Title: US-10-006-922A-11
Perfect score: 678
Sequence: 1 atgaggtcttccaagaatgt.....gccaccatctgtctttaa 678

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002s:*
7: Geneseqn2003as:*
8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	678	100.0	678	4 AAH47654	Aah47654 Discosoma
2	678	100.0	678	4 AAD13053	Aad13053 Discosoma
3	678	100.0	678	4 AAD11142	Aad11142 Discosoma
4	678	100.0	678	6 ABA95921	Abas95921 Yeast opt
5	678	100.0	678	9 ADC24127	Adc24127 Discosoma
6	678	100.0	859	6 AAL47952	Aal47952 Discosoma
7	678	100.0	859	7 AAD53432	Aad53432 Discosoma
8	678	100.0	859	9 AAD61969	Aad61969 Discosoma
9	677	99.9	3311	8 ACA62995	Aca62995 Plasmid D
10	665	98.1	666	6 ABL61142	Ab161142 Red fluor
11	658.8	97.2	898	4 AAD03615	Aad03615 Discosoma
12	657.2	96.9	3	AAA48742	Aaa48742 Discosoma
13	566.4	83.5	876	3 AAA28958	Aaa28958 Discosoma
14	566.4	83.5	876	4 AAD03618	Aad03618 Discosoma
15	566.4	83.5	876	7 ACC44649	Acc44649 Red fluor
16	450.6	66.5	723	7 ABZ22476	Abz22476 Mammalian
17	449.8	66.3	681	4 AAH47656	Aah47656 Anthozoa
18	449.2	66.3	678	6 AAD46278	Aad46278 Discosoma
19	449.2	66.3	678	6 AAD28207	Aad28207 Discosoma
20	449.2	66.3	695	3 AAA48743	Aaa48743 Humanised
21	447.6	66.0	678	6 ABA95922	Abas95922 Yeast opt
22	447.2	66.0	681	9 ADC24134	Adc24134 Discosoma
23	447.2	66.0	4692	6 AAL47954	Aal47954 Modified

24	447.2	66.0	4692	7 ACC44640	Acc44640 Vector pD
25	447.2	66.0	7910	4 AAD09979	Aad09979 pBit(DHSP
26	447.2	66.0	9320	6 ABS56664	Abs56664 Plasmid p
27	446	65.8	678	6 AAD28208	Aad28208 Discosoma
28	445.8	65.8	6893	9 ADE24111	Ade24111 Proviral
29	445.6	65.7	5436	6 AAD10003	Aad10003 Plasmid p
30	441.2	65.1	678	6 ABA95905	Abas95905 Yeast opt
31	441.2	65.1	678	6 ABA95920	Abas95920 Yeast opt
32	439.6	64.8	678	6 AAD28209	Aad28209 Discosoma
33	438.2	64.6	681	6 ABA95906	Abas95906 Yeast opt
34	438.2	64.6	681	6 ABA95907	Abas95907 Yeast opt
35	438	64.6	678	6 AAD46282	Aad46282 Discosoma
36	436.2	64.3	6985	7 ACA55359	Aca55359 Transform
37	435.6	64.2	675	6 AAD46281	Aad46281 Discosoma
38	434.6	64.1	850	4 AAD03614	Aad03614 Discosoma
39	432.2	63.7	678	9 ADC24128	Adc24128 Discosoma
40	410.4	60.5	681	9 ADC24130	Adc24130 Discosoma
41	409.6	60.4	699	4 AAH47653	Aah47653 D. striat
42	409.6	60.4	699	4 AAD13052	Aad13052 Discosoma
43	409.6	60.4	699	4 AAD11141	Aad11141 Discosoma
44	409.6	60.4	960	3 AAA28862	Aaa28862 D. striat
45	404	59.6	404	8 ADA38081	Ada38081 DNA of a

ALIGNMENTS

RESULT 1
AAH47654
ID AAH47654 standard; CDNA; 678 BP.
XX
AC AAH47654;
XX
DT 30-NOV-2001 (first entry)
XX
DE Discosoma sp. red drFP583 protein coding sequence.
XX
KW Fluorescent protein; Anthozoa; fluorescence; marker; FRET; drFP583; ss.
XX
OS Discosoma sp.
XX
PN WO200162919-A1.
XX
PD 30-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-US004625.
XX
PR 23-FEB-2000; 2000US-0184732P.
XX
PA (AURO-) AURORA BIOSCIENCES CORP.
XX
PI Nelson D, Zamaira E, Tsien R,
DR WPI; 2001-557704/62.
XX
PT Proteins for Fluorescence Resonance Energy Transfer (FRET) comprise
PT functional red fluorescent proteins, and the encoding nucleic acids, with
PT key mutations for improving the proteins function.
XX
PS Disclosure; Page 83; 90pp; English.
XX
CC The invention provides a nucleic acid encoding functional red fluorescent
CC protein (II) that differs from the sequence of an Anthozoa red
CC fluorescent protein by at least one amino acid substitution, and with
CC different fluorescent properties. The red fluorescent protein of the
CC invention can be expressed by standard recombinant methodology. (II) are
CC used a fluorescent markers and FRET partners. It is used for identifying
CC protein-protein interactions. (II) is also suitable for multiplexed
CC fluorescent analysis and FRET-based applications using existing Aequeorea
CC fluorescent proteins. (II) has improved brightness, reduced spectral
CC cross talk, and is rapidly and efficiently expressed in mammalian cells.
CC The key mutations in the encoding nucleic acids provide improved folding,
CC brightness, and create (II) with sharper, more defined excitation and

CC emission peaks when expressed in mammalian cells. The present sequence
CC represents the coding sequence of a Discosoma sp. drfp583 protein, an
CC anthozoan fluorescent protein

XX Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
Db 1 ATGAGGCTTCCAGAATGTTATCAAGGAGTTCATGAGGTTTAAAGTTCCGATGGAAGA 60
QY 61 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGAAGAGAGGGGAGGCCATACGAAGGC 120
Db 61 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGAAGAGAGGGGAGGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTGGGATATT 180
Db 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTGGGATATT 180
QY 181 TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATGTCACGACCCCTGCCACATACCA 240
Db 181 TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATGTCACGACCCCTGCCACATACCA 240
QY 241 GACTATAAAAAGCTGTCATTTCTGAAAGATTAAATGGGAAAGGGTCATGAATTGAA 300
Db 241 GACTATAAAAAGCTGTCATTTCTGAAAGATTAAATGGGAAAGGGTCATGAATTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGGATGGCTGTTTCATCTAC 360
Db 301 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGGATGGCTGTTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAAGACA 420
Db 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGCGTGTGGAAGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGCGTGTGGAAGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTAACCTAGTTGAATTCAAAAGTATT 540
Db 481 ATTCAATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTAACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAAAGAGCCCTGTGCAAGCTACCAAGGGTACTACTATGTTGACTCCAAACTGGAT 600
Db 541 TACATGGCAAAAGAGCCCTGTGCAAGCTACCAAGGGTACTACTATGTTGACTCCAAACTGGAT 600
QY 601 ATAACAAGCCACAACGAAAGACTATACATCGTTGAGCAATGAAAGAACCGAGGGAGCGC 660
Db 601 ATAACAAGCCACAACGAAAGACTATACATCGTTGAGCAATGAAAGAACCGAGGGAGCGC 660
QY 661 CACCATCTGTTCTTTAA 678
Db 661 CACCATCTGTTCTTTAA 678

RESULT 2
AADI3053
ID AADI3053 standard; cDNA; 678 BP.
XX
AC AADI3053;
XX
DT 16-OCT-2001 (first entry)
XX
DE Discosoma sp. "red" anthozoa fluorescent protein, drfp583 cDNA.
XX
KM Protein destabilisation; linker moiety; reporter moiety; disease model;
KM linear multimerised domain; -NH-ubiquitin protein endoprotease;
KM transgenic animal; transgenic plant; disease resistance;
KM anthozoa fluorescent protein; natural fluorescent protein; ss.

XX Discosoma sp.
OS
XX WO200157242-A2.
PN
XX 09-AUG-2001.
PD
XX 02-FEB-2001; 2001WO-US003791.
PF
XX 04-FEB-2000; 2000US-00498098.
PR
XX (AURO-) AURORA BIOSCIENCES CORP.
PA
XX Stack JH, Whitney M, Cubitt AB, Pollok BA;
PI
XX WPI; 2001-488890/53.
DR
XX

PT Destabilizing proteins in living cells, by coupling a target protein to
PT linear multimerized destabilization domain non-cleavable by -NH-ubiquitin
PT protein endoproteases, comprising two copies of the domain.

PS Disclosure; Page 110; 171pp; English.

XX The present invention relates to a method for destabilising a target
CC protein in a cell. The method comprises a linker moiety which operatively
CC couples a target protein (a reporter moiety) to a linear multimerised
CC destabilising domain, which is non-cleavable by a -NH-ubiquitin protein
CC endoproteases. The method is useful for detecting an activity such as
CC protease, protein kinase or phosphoprotein phosphatase activity and is
CC also useful for identifying modulators of these activities. The method is
CC also useful for developing novel assays for a wide range of post-
CC translational activities, such as proteolysis, phosphorylation,
CC dephosphorylation, glycosylation, methylation, sulfation, prenylation,
CC disulfide bond formation and ADP-ribosylation within cells. The
CC recombinant DNA molecule of the invention is useful for creating
CC transgenic animals useful as disease models and transgenic plants with
CC improved disease resistance or other favourable traits. The present
CC sequence is Discosoma sp. "red" anthozoa fluorescent protein, drfp483
CC cDNA which is a natural fluorescent protein used as a reporter moiety in
CC the exemplification of the invention

XX Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 4; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAGAATGTTATGCAAGAGTTCATGAGGTTTAAAGTTCCGATGAAGGA 60
Db 1 ATGAGGCTTCCAGAATGTTATGCAAGAGTTCATGAGGTTTAAAGTTCCGATGAAGGA 60
QY 61 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGGAAGAGAGGGGAGGCCATACGAAGGC 120
Db 61 ACGGTCAATGGGCACGAGTTTGAATAGAAAGCGGAAGAGAGGGGAGGCCATACGAAGGC 120
QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTTGGGATATT 180
Db 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGGACCTTTGCCATTGCTTGGGATATT 180
QY 181 TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATATGTCACGACCCCTGCCACATACCA 240
Db 181 TTGTCACCACAATTTCAAGTATGGAAGCAAGGATATATGTCACGACCCCTGCCACATACCA 240
QY 241 GACTATAAAAAGCTGTCATTTCTGAAAGATTAAATGGGAAAGGGTCATGAACCTTGAA 300
Db 241 GACTATAAAAAGCTGTCATTTCTGAAAGATTAAATGGGAAAGGGTCATGAACCTTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
Db 301 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
QY 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAAGACA 420
Db 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAAGACA 420

Db 361 AAGTCAAGTTCATTGGCGTGAACCTTCCCTCCGATGGACCTGTATGCAAAAGAGACA 420
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTGATGCGCGTGTGAAAGGAGAG 480
Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTGATGCGCGTGTGAAAGGAGAG 480
QY 481 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGGTCAATACCTAGTTGAATTCAAAAGTATT 540
Db 481 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGGTCAATACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTATGTTGACTCCAAACTGGAT 600
Db 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTATGTTGACTCCAAACTGGAT 600
QY 601 ATAACAAGCCACAAGAGACTATACAATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660
Db 601 ATAACAAGCCACAAGAGACTATACAATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660
QY 661 CACCATCTGTCTCTTAA 678
Db 661 CACCATCTGTCTCTTAA 678

RESULT 3

AAD11142
ID AAD11142 standard; DNA; 678 BP.

AC AAD11142;

DT 24-SEP-2001 (first entry)

DE Discosoma species Anthozoa fluorescent protein, drFP583 encoding DNA.

KW Transmembrane potential; biological membrane; fluorescent ion; detection;
test chemical screening; Anthozoa fluorescent protein; FP;
transgenic organism; drFP583 protein; ds.

OS Discosoma sp.

PN WO200142211-A2.

PD 14-JUN-2001.

PF 12-DEC-2000; 2000WO-US033739.

PR 13-DEC-1999; 99US-00459956.

PA (REGC) UNIV CALIFORNIA.

PI Tsien RY, Gonzalez JE;

DR WPI; 2001-457276/49.

PT Determining electrical potential across a membrane in biological systems,
comprises introducing two reagents, exposing the membrane to light and
measuring the energy transfer.

PS Disclosure; Page 150; 154pp; English.

CC The patent discloses optical methods and compositions for determining
transmembrane potential across biological membranes in living cells. The
method of determining the electrical potential across a membrane in a
biological system comprises introduction of two reagents, a first reagent
comprising a hydrophobic fluorescent ion capable of redistributing from a
first face of the membrane to a second face of the membrane in response
to membrane potential change and a second reagent that label the first
face or the second face of the membrane, which comprises a chromophore
capable of undergoing energy transfer by either donating or accepting
excited state energy to the fluorescent ion. The membrane is then exposed
to excitation light and the energy transfer between the reagents is
measured and related to the membrane potential. The method is useful for
detecting changes in membrane potential in subcellular organelle
membranes in biological systems. The method is used for screening of test

CC chemicals for activity to modulate the activity of target ion channel.
CC The invention also provides a transgenic organism comprising a first
CC reagent that comprises a charged hydrophobic fluorescent molecule and a
CC second reagent comprising a bioluminescent or naturally fluorescent
CC protein. The present sequence is Discosoma species (red) DNA encoding an
CC Anthozoa fluorescent protein (FP), drFP583

XX Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 678; DB 4; Length 678;

Best Local Similarity 100.0%; Pred. No. 7.3e-208;

Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAGAATGTTATCAAGAGTTCATGAGGTTTAAAGTTGCGATGGAAGGA 60

Db 1 ATGAGGCTTCCAGAATGTTATCAAGAGTTCATGAGGTTTAAAGTTGCGATGGAAGGA 60

QY 61 ACGGTCAATGGGCACGAGTTTGAATAAGGCGGAAGGAGAGGGAGCCATACGAAGGC 120

Db 61 ACGGTCAATGGGCACGAGTTTGAATAAGGCGGAAGGAGAGGGAGCCATACGAAGGC 120

QY 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGACCTTGGCATTGCTTGGATATT 180

Db 121 CACAATACCGTAAAGCTTAAGGTAACCAAGGGGACCTTGGCATTGCTTGGATATT 180

QY 181 TTGTCAACCAATTTCAATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240

Db 181 TTGTCAACCAATTTCAATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240

QY 241 GACTATAAAAAGCTGTCAATTCCTGAAAGATTAAATGGGAAAGGTCATGAACCTTGA 300

Db 241 GACTATAAAAAGCTGTCAATTCCTGAAAGATTAAATGGGAAAGGTCATGAACCTTGA 300

QY 301 GACGCTGGCGTCTGTTACTGTAAACCCAGGATTCAGTTGCAAGATGGCTGTTTCATCTAC 360

Db 301 GACGCTGGCGTCTGTTACTGTAAACCCAGGATTCAGTTGCAAGATGGCTGTTTCATCTAC 360

QY 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAGACA 420

Db 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCCTCCGATGACCTGTTATGCAAAAGAGACA 420

QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTATGCGGCGTGTGAAGAGAGAG 480

Db 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTATGCGGCGTGTGAAGAGAGAG 480

QY 481 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTTACCTAGTTGAATCAAAAGTATT 540

Db 481 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTTACCTAGTTGAATCAAAAGTATT 540

QY 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTATGTTGACTCCAAACTGGAT 600

Db 541 TACATGGCAAGAAGCCTGTGACGCTACAGGGTACTACTATGTTGACTCCAAACTGGAT 600

QY 601 ATAACAAGCCACAAGAGACTATACAATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660

Db 601 ATAACAAGCCACAAGAGACTATACAATCGTTGAGCAGTATGAAGAAGCCGAGGAGCGC 660

QY 661 CACCATCTGTCTCTTAA 678

Db 661 CACCATCTGTCTCTTAA 678

QY 661 CACCATCTGTCTCTTAA 678

Db 661 CACCATCTGTCTCTTAA 678

AC ABA95921;

DT 29-MAY-2002 (first entry)

DE Yeast optimised RFP related DNA SEQ ID NO 18.

KW Yeast; red fluorescent protein; RFP; plant; transgenic; GFP;

KW Saccharomyces cerevisiae; Nicotiana tabacum; Arabidopsis thaliana; Escherichia coli; green fluorescent protein; biotechnology; gene; ss.
XX Anthozoa.
XX Key Location/Qualifiers
FH 1. .678
FT CDS /*tag= a
FT /product= "yeast optimised Red Fluorescent Protein"
XX DE20001395-U1.
XX PD 15-MAR-2001.
XX PF 27-JAN-2000; 2000DE-02001395.
XX PR 27-JAN-2000; 2000DE-02001395.
XX PA (GPCB-) GPC BIOTECH AG.
XX DR WPI; 2002-228394/29.
XX DR P-PSDB; ABB08834.
XX PT New DNA encoding red fluorescent protein, useful as marker in
PT biotechnology, has sequence optimized for expression in eukaryotes,
PT especially yeast or plants.
XX PS Disclosure; Page 14; 19pp; German.
XX CC The invention relates to DNA (I) containing either sequence ABA95905 or
CC sequence ABA95906 encoding a yeast optimised Red Fluorescent Protein
CC (yRFP). (I) are used to express red fluorescent protein (RFP) in
CC eukaryotes, especially yeast, especially Saccharomyces cerevisiae and
CC plants, especially dicotyledonous plants including Nicotiana tabacum or
CC Arabidopsis thaliana and also in prokaryotes, especially bacteria,
CC especially Escherichia coli. RFP is useful in the same way as green
CC fluorescent protein but is more generally applicable in modern
CC biotechnology. (I) are optimised for expression in yeast and so generate
CC RFP at higher levels with stronger fluorescence and thus lowers the
CC detection limit and gives a better signal-to-noise ratio. The present
CC sequence is that of a polynucleotide encoding the yeast optimised RFP,
CC useful to the invention
XX SQ Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;
Query Match 100.0%; Score 678; DB 6; Length 678;
Best Local Similarity 100.0%; Pred.No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 ATGAGGTCTTCCAGAATGTTATCAAGAGTTCATGAGCTTTAAGTTCGATGGAAGA 60
DB 1 ATGAGGTCTTCCAGAATGTTATCAAGAGTTCATGAGCTTTAAGTTCGATGGAAGA 60
QY 61 ACGGTCAATGGGCAAGGTTGAATAGAAAGCGCAAGAGAGGGGAGGCCATACGAAGGC 120
DB 61 ACGGTCAATGGGCAAGGTTGAATAGAAAGCGCAAGAGAGGGGAGGCCATACGAAGGC 120
QY 121 CACAATACCGTTAAGCTTAAGGTAAACCAAGGGGGACCTTGGCATTGCTGGGATATT 180
DB 121 CACAATACCGTTAAGCTTAAGGTAAACCAAGGGGGACCTTGGCATTGCTGGGATATT 180
QY 181 TTGTCAACCAATTTACATATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240
DB 181 TTGTCAACCAATTTACATATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240
QY 241 GACTATAAAAGCTGTCAATTCCTGAAGGATTTAAATGGGAAAGGTCATGAATTTGAA 300
DB 241 GACTATAAAAGCTGTCAATTCCTGAAGGATTTAAATGGGAAAGGTCATGAATTTGAA 300
QY 301 GACGGTGGCGTCTACTGTAAACCCAGGATTCAGTTGCAAGGATGGCTGTTCACTAC 360
DB 301 GACGGTGGCGTCTACTGTAAACCCAGGATTCAGTTGCAAGGATGGCTGTTCACTAC 360

QY 361 AAGTCAAGTTCAATGGCGTGAACCTTCCCTCCGATGAGACCTGTTATGCAAAAGAGACA 420
DB 361 AAGTCAAGTTCAATGGCGTGAACCTTCCCTCCGATGAGACCTGTTATGCAAAAGAGACA 420
QY 421 ATGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTGAAGCGGTGTTGAAAGAGAG 480
DB 421 ATGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTGAAGCGGTGTTGAAAGAGAG 480
QY 481 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATCCAAGATATT 540
DB 481 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATCCAAGATATT 540
QY 541 TACATGGCAAGAAAGCCTGTGACGCTACCAAGGCTACTATATGTTGACTCCAACTGAT 600
DB 541 TACATGGCAAGAAAGCCTGTGACGCTACCAAGGCTACTATATGTTGACTCCAACTGAT 600
QY 601 ATAACAAGCCACAACGAAGACTATACATCGTTGACAGATATGAAGAACGAGGAGCGC 660
DB 601 ATAACAAGCCACAACGAAGACTATACATCGTTGACAGATATGAAGAACGAGGAGCGC 660
QY 661 CACCATCTGTTCCCTTTAA 678
DB 661 CACCATCTGTTCCCTTTAA 678

RESULT 5
ADC24127
ID ADC24127 standard; DNA; 678 BP.
XX AC ADC24127;
XX DT 18-DEC-2003 (first entry)
XX DE Discosoma wild-type red fluorescent protein DNA #1.
XX KW Discosoma red fluorescent protein; DsRed; AB interface; AC interface;
KW fluorescent protein variant; transcription induction detection;
KW fluorescence energy resonance transfer; FRET; protein kinase;
KW protein phosphatase; ion indicator; ds.
XX OS Discosoma.
XX PN US2003059835-A1.
XX PD 27-MAR-2003.
XX PF 10-APR-2002; 2002US-00121258.
XX PR 26-FEB-2001; 2001US-00794308.
XX PR 24-MAY-2001; 2001US-00866538.
XX PA (TSIE/) TSIE R Y.
XX PA (CAMP/) CAMPBELL R E.
XX PI Tsien RY, Campbell RE;
XX DR WPI; 2003-743764/70.
XX DR P-PSDB; ADC24126.
XX PT Novel polynucleotide sequence encoding Discosoma red fluorescent protein
PT variant having a reduced propensity to oligomerize, useful for detecting
PT transcriptional activity.
XX PS Example 1; SEQ ID NO 2; 67pp; English.
XX CC The invention describes a polynucleotide sequence (I) encoding a
CC Discosoma red fluorescent protein (DsRed) variant having a reduced
CC propensity to oligomerise, comprising amino acid substitutions at the AB
CC and/or AC interfaces of the wild-type DsRed sequence (S1) comprising 225
CC amino acids, given in the specification, where the substitutions result
CC in reduced propensity of the DsRed variant to form tetramers. (I) is
CC useful for detecting transcriptional activity by providing a host cells
CC containing a vector which comprises (I) operatively linked to an

CC expression control sequence, and an unit to assay the variant fluorescent
CC protein fluorescence, and assaying fluorescence of the variant
CC fluorescent protein produced by (VII), where variant fluorescent protein
CC fluorescence is indicative of transcriptional activity. A polynucleotide
CC encoding a fusion protein is useful for the analysis of in vivo
CC localisation or trafficking of a polypeptide of interest. A polypeptide
CC marker is useful as markers to identify the location and amount of a
CC target protein produced, where the target protein is fused to the marker,
CC as a complement to or alternative for the green fluorescent protein or
CC its spectral variant, for detecting induction of transcriptions, in
CC applications involving fluorescence energy resonance transfer (FRET),
CC which detects events as the function of the movement of fluorescent
CC donors and acceptors towards or away from each other, for making
CC fluorescent sensors for protein kinase and phosphatase activities or
CC indicators for ions and molecules such as Ca2+, Zn2+, for identifying the
CC presence of a molecule in a sample, for identifying a specific
CC interaction of a first and second molecule, for determining whether a
CC sample contains an enzyme or for determining the pH of the sample. (I) is
CC useful for identifying a region or condition that regulates the activity
CC of an expression control sequence. This sequence encodes Discosoma wild-
CC type red fluorescent protein.

XX
XX
SQ Sequence 678 BP; 205 A; 129 C; 178 G; 166 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 9; Length 678;
Best Local Similarity 100.0%; Pred. No. 7.3e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTTCGATGGAAGA 60
DB 1 ATGAGGCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTTCGATGGAAGA 60
QY 61 ACGGTCAATGGGACGAGTTTGAATAGAAAGCGAAGAGAGAGGGGCCATACGAAGGC 120
DB 61 ACGGTCAATGGGACGAGTTTGAATAGAAAGCGAAGAGAGAGGGGCCATACGAAGGC 120
QY 121 CACAATACCGTAAGCTTAAGSTAACCAAGGGGGACCTTGGCATTTGCTTGGATATT 180
DB 121 CACAATACCGTAAGCTTAAGSTAACCAAGGGGGACCTTGGCATTTGCTTGGATATT 180
QY 181 TTGTACCAACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
DB 181 TTGTACCAACAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
QY 241 GACTATATAAAAGCTGTCTATTCCTGAAGATTTAAATGGAAAGGCTCATGAACCTTTGAA 300
DB 241 GACTATATAAAAGCTGTCTATTCCTGAAGATTTAAATGGAAAGGCTCATGAACCTTTGAA 300
QY 301 GACGGTGGCGTCTTACTGTAAACCCAGAGTTCCAGTTTGACAGATGGCTTTCATCTAC 360
DB 301 GACGGTGGCGTCTTACTGTAAACCCAGAGTTCCAGTTTGACAGATGGCTTTCATCTAC 360
QY 361 AAGGTCAAGTTTCATTTGGCGTGAACCTTCCGATGAGCCCTGTATGCAAAAGAAGACA 420
DB 361 AAGGTCAAGTTTCATTTGGCGTGAACCTTCCGATGAGCCCTGTATGCAAAAGAAGACA 420
QY 421 ATGGGCTGGGAAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGGTGTAAGAGAGAG 480
DB 421 ATGGGCTGGGAAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGGTGTAAGAGAGAG 480
QY 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGCTGTCATTACCTAGTTGAATTCAAAAGTATT 540
DB 481 ATTCAATAAGGCTCTGAAGCTGAAAGACGCTGTCATTACCTAGTTGAATTCAAAAGTATT 540
QY 541 TACATGGCAAGAAGCCTGTGACGCTAACAGGGTACTACTATGTTGACTCCAAACTGAT 600
DB 541 TACATGGCAAGAAGCCTGTGACGCTAACAGGGTACTACTATGTTGACTCCAAACTGAT 600
QY 601 ATAACAAGCCACAACGAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
DB 601 ATAACAAGCCACAACGAGACTATACATCGTTGAGCAGTATGAAGAACCAGAGGAGCC 660
QY 661 CACCATCTGTTCTTTAA 678

DB 661 CACCATCTGTTCTTTAA 678
RESULT 6
AAL47952
ID AAL47952 standard; DNA; 859 BP.
AC AAL47952;
XX 26-SEP-2002 (first entry)
DT 26-SEP-2002 (first entry)
XX Discosoma red fluorescent protein coding sequence.
DE Discosoma red fluorescent protein coding sequence.
XX Yeast; RAD54; promoter; genotoxicity cassette; cytotoxicity cassette;
KW modified yeast strain; environmental pollution; gene; ds.
XX Discosoma sp.
OS Discosoma sp.
XX Key Location/Qualifiers
FH CDS 54..731
FT /*tag= a
FT /product= "red fluorescent protein"

PN DE1061872-A1.
XX 20-JUN-2002.
PD 20-JUN-2002.
XX 12-DEC-2000; 2000DE-01061872.
PF 12-DEC-2000; 2000DE-01061872.
XX 12-DEC-2000; 2000DE-01061872.
PR (LICH/) LICHTENBERG-FRATE H.
XX Lichtenberg-Frate H.
PI
XX WPI; 2002-539633/58.
DR P-PSDB; AAO18270.
XX
XX Modified yeast strain, useful for detecting toxic compounds in
PT environment, contains integrated cassettes responsive to genotoxic and
PT cytotoxic compounds.
XX
XX Disclosure; Page 20-21; 34pp; German.
PS
XX The present invention relates to a modified yeast strain that contains,
CC integrated stably and functionally in its genome, a genotoxicity cassette
CC and a cytotoxicity cassette, each comprising a promoter and reporter
CC gene, both of which are different in the two cassettes. The modified
CC yeast strain is used to detect environmental pollution, especially
CC genotoxic and/or cytotoxic substances in complex environmental
CC contaminants, especially organic compounds, but also (non-)ionising
CC radiation and chemical carcinogens. Particular applications are in
CC monitoring (waste) water (e.g. as an early warning system), medical
CC toxicology screening and for industrial process control. The present
CC sequence is a marker gene suitable for use in the cassettes of the
CC present invention
XX
SQ Sequence 859 BP; 263 A; 163 C; 228 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 6; Length 859;
Best Local Similarity 100.0%; Pred. No. 8.2e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTTCGATGGAAGA 60
DB 54 ATGAGGCTTCCAAGATGTTATCAAGAGTTCATGAGGTTTAAAGTTTCGATGGAAGA 113
QY 61 ACGGTCAATGGGACGAGTTTGAATAGAAAGCGAAGAGAGGGGCCATACGAAGGC 120
DB 114 ACGGTCAATGGGACGAGTTTGAATAGAAAGCGAAGAGAGGGGCCATACGAAGGC 173
QY 121 CACAATAACCGTAAGCTTAAGSTAACCAAGGGGGACCTTTGCCATTTGCTTGGATATT 180

|||||
Db 174 CACAATACCGTAAGCTTAAGCTAACCAAGGGGGACCTTTGCCATTTGCTGGGATATT 233
QY 181 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
Db 234 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 293
QY 241 GACTATAAAAGCTGTCAATTTCTGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 300
Db 294 GACTATAAAAGCTGTCAATTTCTGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 353
QY 301 GACGGTGGCGTCTGTAAGTAAACCCAGGATCCAGTTTGACAGGATGGCTGTTTCACTAC 360
Db 354 GACGGTGGCGTCTGTAAGTAAACCCAGGATCCAGTTTGACAGGATGGCTGTTTCACTAC 413
QY 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAGACA 420
Db 414 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGTGTGAAAGAGAG 480
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGTGTGAAAGAGAG 533
QY 481 ATTCAATAGGCTCTGAAGCTGAAAGACGTTGCTATTACCTAGTTGAATTCAAAAGTATT 540
Db 534 ATTCATAAGGCTCTGAAGCTGAAGACGGTGGTCACTTAAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCGCTGTGCAGCTACCAGGGTACTACTATGTGACTCCAAACTGGAT 600
Db 594 TACATGGCAAGAAGCGCTGTGCAGCTACCAGGGTACTACTATGTGACTCCAAACTGGAT 653
QY 601 ATAACAAGCCACAACGAACTATACAATCGTTGACAGATATGAAGAACCGAGGAGCGC 660
Db 654 ATAACAAGCCACAACGAACTATACAATCGTTGACAGATATGAAGAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTAA 678
Db 714 CACCATCTGTTCTTTAA 731

RESULT 7
AAD53432
ID AAD53432 standard; DNA; 859 BP.
XX AAD53432;
AC AAD53432;
XX 28-MAY-2003 (first entry)
DT 28-MAY-2003 (first entry)
XX
DE Discosoma species red fluorescent protein (RFP) encoding DNA.
XX
KM Phosphorylation indicator; fluorescent protein; detection; phosphatase;
KW kinase; red fluorescent protein; RFP; gene; ds.
XX
OS Discosoma sp.
XX
FH Key Location/Qualifiers
FT CDS 54..731
FT /*tag= a
FT /product= "Discosoma sp. red fluorescent protein (RFP)"
XX
PN WO200295058-A2.
XX
PD 28-NOV-2002.
XX
XX 24-MAY-2002; 2002WO-US016955.
PF 24-MAY-2001; 2001US-00865291.
XX
PR 24-MAY-2001; 2001US-00865291.
XX
PA (REGC) UNIV CALIFORNIA.
XX
XX Tsien RY, Ting AY, Zhang J;
PI
XX
DR WPI; 2003-148474/14.

DR P-PSDB; AAE34962.
XX
PT Novel chimeric phosphorylation indicators, useful for detecting
PT kinase/phosphatase in samples, has donor molecule, phosphorylatable
PT domain, phosphoaminoacid binding domain, and acceptor molecule, in
PT operative linkage.
XX
PS Disclosure; Col 64-65; 38pp; English.
XX
CC The present invention relates to chimeric phosphorylation indicators
CC comprising a phosphorylation polypeptide and a fluorescent protein or in
CC operative linkage, a donor molecule, a phosphorylatable domain, a
CC phosphoaminoacid binding domain (PABD) and an acceptor molecule. The
CC phosphorylation indicators of the invention are useful for detecting
CC kinases or phosphatases in a biological sample. They are also useful in
CC high throughput analysis e.g. for detecting a kinase inhibitor or
CC phosphatase inhibitor. The present sequence is Discosoma species red
CC fluorescent protein (RFP) encoding DNA used in the invention
XX
SQ Sequence 859 BP; 263 A; 163 C; 228 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 7; Length 859;
Best Local Similarity 100.0%; Pred. No. 8.2e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTTCATGAGGTTTAAAGTTCCGATGAAGGA 60
Db 54 ATGAGGCTTCCAAAGATGTTATCAAGAGTTTCATGAGGTTTAAAGTTCCGATGAAGGA 113
QY 61 ACGGTCAATGGGCAAGAGTTTGAATAGAGCGGAAGAGAGGGGAGGCCATACGAAGGC 120
Db 114 ACGGTCAATGGGCAAGAGTTTGAATAGAGCGGAAGAGAGGGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGGTAAGCTTAAGGTAAACCAAGGGGAGCCTTTGCCATTGCTTGGGATATT 180
Db 174 CACAATACCGGTAAGCTTAAGGTAAACCAAGGGGAGCCTTTGCCATTGCTTGGGATATT 233
QY 181 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
Db 234 TTGTCAACCACAATTTAGTATGGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 293
QY 241 GACTATAAAAGCTGTCAATTTCTGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 300
Db 294 GACTATAAAAGCTGTCAATTTCTGAAGATTTAAATGGGAAAGGTCATGAACCTTGAA 353
QY 301 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGATGGCTGTTTCACTAC 360
Db 354 GACGGTGGCGTCTTACTGTAACCCAGGATTCAGTTTGACAGATGGCTGTTTCACTAC 413
QY 361 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAGACA 420
Db 414 AAGGTCAAGTTCATTGGCGGTGAACCTTCCGATGGAACCTGTTATGCAAAAGAGACA 473
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGTGTGAAAGAGAG 480
Db 474 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGTGTGAAAGAGAG 533
QY 481 ATTCAATAGGCTCTGAAGCTGAAAGACGGTGGTCACTTACCTAGTTGAATTCAAAAGTATT 540
Db 534 ATTCAATAGGCTCTGAAGCTGAAAGACGGTGGTCACTTACCTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAGAAGCGCTGTGCAGCTACAGGTAAGTACTATGTTGACTCCAAACTGGAT 600
Db 594 TACATGGCAAGAAGCGCTGTGCAGCTACAGGTAAGTACTATGTTGACTCCAAACTGGAT 653
QY 601 ATAACAAGCCACAACGAACTATACAATCGTTGACAGATATGAAGAACCGAGGAGCGC 660
Db 654 ATAACAAGCCACAACGAACTATACAATCGTTGACAGATATGAAGAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTAA 678
Db 714 CACCATCTGTTCTTTAA 731

```
RESULT 8
AAD61969
ID AAD61969 standard; cDNA; 859 BP.
XX
AC AAD61969;
XX
DT 15-JAN-2004 (first entry)
XX
DE Discosoma sp. red fluorescent protein (RFP) cDNA.
XX
KW Fluorescent protein; resonance energy transfer; pH; detection;
KW red fluorescent protein; RFP; gene; ss.
XX
OS Discosoma sp.
XX
FH Key Location/Qualifiers
FT CDS 54..731
FT /*tag= a
FT /product= "Discosoma sp. red fluorescent protein"
XX
PN US2003170911-A1.
XX
PD 11-SEP-2003.
XX
PF 26-FEB-2001; 2001US-00794308.
XX
PR 26-FEB-2001; 2001US-00794308.
XX
PA (TSIE/) TSIE R Y.
PA (ZACH/) ZACHARIAS D A.
PA (BAIR/) BAIRD G S.
XX
PI Tsien RY, Zacharias DA, Baird GS;
XX
DR WPI; 2003-802418/75.
DR P-PSDB; ABW00918.
XX
PT Fluorescent proteins containing a mutation that reduces or eliminates its
PT ability to oligomerize which gives more reliable fluorescence resonance
PT energy transfer results and are useful to detect molecule interaction,
PT enzymes, or sample pH.
XX
PS Disclosure; Page 29-30; 0pp; English.
XX
CC The invention relates to a non-oligomerising fluorescent protein
CC containing a mutation that reduces or eliminates its ability to
CC oligomerise. The fluorescent protein gives more reliable fluorescence
CC resonance energy transfer results and are useful to detect molecule
CC interaction, enzymes, or sample pH. These are also used to identify
CC agents or conditions that regulate expression of control sequences. The
CC present sequence is Discosoma sp. red fluorescent protein (RFP) cDNA
XX
SQ Sequence 859 BP; 263 A; 163 C; 228 G; 205 T; 0 U; 0 Other;

Query Match 100.0%; Score 678; DB 9; Length 859;
Best Local Similarity 100.0%; Pred. No. 8.2e-208;
Matches 678; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGTCTTCCAAGATGTATCAAGAGTTTCATGAGGTTTAAGTTTCGCATGAAGCA 60
DB 54 ATGAGGTCTTCCAAGATGTATCAAGAGTTTCATGAGGTTTAAGTTTCGCATGAAGCA 113
QY 61 ACGGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGGCCATACGAAGGC 120
DB 114 ACGGTCAATGGGACGAGTTTGAATATGAAGCGGAAGAGAGGGGAGGCCATACGAAGGC 173
QY 121 CACAATACCGTAAGCTTAAGGTAACCAAGGGGGACCTTTGGCCATTGCTTGGATATT 180
DB 174 CACAATACCGTAAGCTTAAGGTAACCAAGGGGGACCTTTGGCCATTGCTTGGATATT 233
QY 181 TTGTACCACAATTTAGTATGAAGCAAGGTATATGTCAAGCACCTGCGCATACCA 240
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DB 234 TTGTACCACAATTTAGTATGAAGCAAGGTATATGTCAAGCACCTGCGCATACCA 293
QY 241 GACTATAAAAGCTGTCAATTTCTGAAGATTTAATGGAAAGGTCATGAACCTTGAA 300
DB 294 GACTATAAAAGCTGTCAATTTCTGAAGATTTAATGGAAAGGTCATGAACCTTGAA 353
QY 301 GACGTGGCGTCGTTACTGTATACCCAGGATTCCAGTTTGCAGATGGCTGTTTCATCTAC 360
DB 354 GACGTGGCGTCGTTACTGTATACCCAGGATTCCAGTTTGCAGATGGCTGTTTCATCTAC 413
QY 361 AAGGTCAAGTTCATTGGCGTGAACCTTCTCCGATGAGCTGTTATGCCAAAAGAGACA 420
DB 414 AAGGTCAAGTTCATTGGCGTGAACCTTCTCCGATGAGCTGTTATGCCAAAAGAGACA 473
QY 421 ATGGCTGGGAAGCCAGCACTGACGCTTTGTATCCCTCGATGGCGGTTGAAAGGAGAG 480
DB 474 ATGGCTGGGAAGCCAGCACTGACGCTTTGTATCCCTCGATGGCGGTTGAAAGGAGAG 533
QY 481 ATTCATAAGGCTCTGAAGCTGAAGACGGTGTCACTTACCTAGTTGAATTCAAAAGTATT 540
DB 534 ATTCATAAGGCTCTGAAGCTGAAGACGGTGTCACTTACCTAGTTGAATTCAAAAGTATT 593
QY 541 TACATGGCAAAAGAGCCCTGTGCACTACCAAGGTTACTATGTGACTCCAAACTGGAT 600
DB 594 TACATGGCAAAAGAGCCCTGTGCACTACCAAGGTTACTATGTGACTCCAAACTGGAT 653
QY 601 ATAACAGCCCAACGAGACTATACATCGTTGAGCAGATGAAGAACCGAGGAGCGC 660
DB 654 ATAACAGCCCAACGAGACTATACATCGTTGAGCAGATGAAGAACCGAGGAGCGC 713
QY 661 CACCATCTGTTCTTTAA 678
DB 714 CACCATCTGTTCTTTAA 731

RESULT 9
ACA62995
ID ACA62995 standard; DNA; 3311 BP.
XX
AC ACA62995;
XX
DT 23-SEP-2003 (first entry)
XX
DE Plasmid DNA containing coding sequence for RFP.
XX
KW Fluorescently-tagged enzyme; substrate; cell population; GFP;
KW quantification of enzymatic activity; green fluorescent protein; EGFP;
KW red fluorescent protein; RFP; enhanced green fluorescent protein;
KW enzymatic process; cellular enzyme; chemotherapeutic drug;
KW multidrug resistance; MDR; ds.
XX
OS Aequorea victoria.
OS Synthetic.
XX
PN US2003049597-A1.
XX
PD 13-MAR-2003.
XX
PF 01-MAR-2001; 2001US-00797496.
XX
PR 01-MAR-2001; 2001US-00797496.
XX
PA (SIMO/) SIMON S M.
PA (CHEN/) CHEN Y.
XX
PI Simon SM, Chen Y;
XX
DR WPI; 2003-555145/52.
XX
PT Simultaneously quantifying in situ the relationship between an enzyme and
PT its substrate for study of enzymatic processes at a cellular level,
PT comprises optical measurements on cells expressing the fluorescently
PT tagged enzyme.
```


XX Disclosure; Page 8-9; 21pp; English.
PS
XX
CC The present invention relates to a method for simultaneously quantifying
CC in situ the relationship between a fluorescently-tagged enzyme (E) and
CC its substrate in a population of cells. A population of cells expressing
CC (E) is created in which different cells contain different amounts of (E).
CC The cells are incubated with a substrate, and the concentration and
CC enzymatic activity of (E) in each cell are simultaneously quantified by
CC optical means. The fluorescently-tagged enzyme is produced by linking the
CC enzyme with Aequorea victoria green fluorescent protein (GFP), or its
CC variants or derivatives such as red fluorescent protein (RFP) and
CC enhanced green fluorescent protein (EGFP). The method of the invention is
CC useful for simultaneously quantifying in situ the relationship between an
CC enzyme and its substrate in a cell. The method is useful for the study of
CC enzymatic processes at the cellular level, and especially for examining
CC the interactions of cellular enzymes with chemotherapeutic drugs, e.g.
CC for elucidating mechanisms of multidrug resistance (MDR). The present
CC sequence represents a plasmid containing the coding sequence for RFP
XX
SQ Sequence 3311 BP; 858 A; 778 C; 860 G; 815 T; 0 U; 0 Other;

Query Match 99.9%; Score 677; DB 8; Length 3311;
Best Local Similarity 100.0%; Pred. No. 3.4e-207;
Matches 677; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGGCTTCCAGAAATGTTATCAAGGAGTTCATGAGGTTAAGGTTCCGATGGAAGGA 60
DB 289 ATGAGGCTTCCAGAAATGTTATCAAGGAGTTCATGAGGTTAAGGTTCCGATGGAAGGA 348

QY 61 ACGGTCAATGGGCACGAGTTTGAATAGAAGGCGAAGAGGGGAGGCCATACGAAGGC 120
DB 349 ACGGTCAATGGGCACGAGTTTGAATAGAAGGCGAAGAGGGGAGGCCATACGAAGGC 408

QY 121 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGGACCTTTGCCATTTGCTGGATATT 180
DB 409 CACAATACCGTAAAGCTTAAAGTAACCAAGGGGGGACCTTTGCCATTTGCTGGATATT 468

QY 181 TTGTCAACCACAATTTGAGTATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 240
DB 469 TTGTCAACCACAATTTGAGTATGGAAGCAAGGTAATGTCAAGCACCCCTGCCACATACCA 528

QY 241 GACTATAAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGGTCATGAACCTTGAA 300
DB 529 GACTATAAAAGCTGTCAATTTCTGGAAGATTAAATGGGAAAGGGTCATGAACCTTGAA 588

QY 301 GACGGTGGCGTCTTACTGTAAACCCAGGATCCAGTTTGCAGGATGGCTGTTTCATCTAC 360
DB 589 GACGGTGGCGTCTTACTGTAAACCCAGGATCCAGTTTGCAGGATGGCTGTTTCATCTAC 648

QY 361 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGACCTGTTAAGCAAAAGAAGACA 420
DB 649 AAGGTCAAGTTCAATGGCGTGAACCTTCCGATGGACCTGTTAAGCAAAAGAAGACA 708

QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGTGTGAAGAAGAG 480
DB 709 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGTGTGAAGAAGAG 768

QY 481 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCAATTAACCTAGTTGAATCAAAAGTATT 540
DB 769 ATTCATAAGGCTCTGAAGCTGAAGAAGCGGTGTCAATTAACCTAGTTGAATCAAAAGTATT 828

QY 541 TACATGGCAAGAAGCGCTGTGCAAGCTACCAAGGTAATACTATGTGACTCCAAACTGGAT 600
DB 829 TACATGGCAAGAAGCGCTGTGCAAGCTACCAAGGTAATACTATGTGACTCCAAACTGGAT 888

QY 601 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 660
DB 889 ATAACAAGCCACAACGAGACTATACAATCGTTGAGCAGTATGAAGAAGCGAGGAGCGC 948

QY 661 CACCATCTGTTCTTTA 677
DB 949 CACCATCTGTTCTTTA 965

RESULT 10
ABL61142
ID ABL61142 standard; DNA; 666 BP.
XX
AC ABL61142;
XX
DT 18-SEP-2002 (first entry)
XX
DE Red fluorescent protein reporter DNA fragment.
XX
KW Alpha-SMA; smooth muscle actin; screening; smooth muscle cell;
KW myofibroblast; gene therapy; red fluorescent protein; ds.
XX
OS Synthetic.
XX
PN EP1172375-A1.
XX
PD 16-JAN-2002.
XX
PF 22-DEC-2000; 2000EP-00128446.
XX
PR 11-JUL-2000; 2000DE-01033633.
PR 31-OCT-2000; 2000DE-01053879.
XX
PA (ODEN/) ODONTAL M.
XX
PI Odenthal M, Jung D;
XX
DR WPI; 2002-149590/20.
XX
PT New nucleic acid containing regulatory region of the smooth muscle actin
PT gene, useful e.g. for manipulating gene expression in smooth muscle
PT cells.
XX
PS Disclosure; Page 20; 44pp; German.
XX
CC This invention describes a novel nucleic acid (I) comprising: (i) at
CC least one functional region (Ia) from the regulatory region of the alpha-
CC smooth muscle actin (SMA) gene and (ii) at least one additional
CC functional sequence (Ib) operably linked to (Ia). The products of the
CC invention can be used for preparing genetically modified eukaryotic cells
CC or organisms, for isolation and screening of smooth muscle cells,
CC myofibroblasts or related cells, and for manipulation of gene expression
CC and/or cell function in smooth muscle cell or myofibroblasts,
CC particularly for gene therapy. Component (Ia) provides cell-type- or
CC differentiation-specific expression or modulation of genes. This sequence
CC represents a DNA fragment of red fluorescent protein (EGFP) which can be
CC used as a reporter molecule under the control of the alpha-SMA described
CC in the invention
XX
SQ Sequence 666 BP; 202 A; 126 C; 176 G; 162 T; 0 U; 0 Other;

Query Match 98.1%; Score 665; DB 6; Length 666;
Best Local Similarity 100.0%; Pred. No. 1.1e-203;
Matches 665; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AAGAATGTTATCAAGAGTTCATGAGCTTTAAGGTTCCGATGGAAGAACGTCATGGG 72
DB 1 AAGAATGTTATCAAGAGTTCATGAGCTTTAAGGTTCCGATGGAAGAACGTCATGGG 60

QY 73 CACGAGTTGAAATAGAAAGCGGAAGAGAGGGAGGCCATACGAAGGCCACAATACCGTA 132
DB 61 CACGAGTTGAAATAGAAAGCGGAAGAGAGGGAGGCCATACGAAGGCCACAATACCGTA 120

QY 133 AAGCTTAAGGTAACCAAGGGGGGACCTTGGCCATTGCTGGGATATTTGTCAACACAA 192
DB 121 AAGCTTAAGGTAACCAAGGGGGGACCTTGGCCATTGCTGGGATATTTGTCAACACAA 180

QY 193 TTTCAAGTGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACAGACTATAAAAG 252
DB 181 TTTCAAGTGAAGCAAGGTATATGTCAAGCACCCCTGCCGACATACAGACTATAAAAG 240

QY 253 CTGTCATTTCCTGAAGGATTTAAATGGGAAGGTCATGAACCTTTGAAGCGGTGGCGTC 312
DB 241 CTGTCATTTCCTGAAGGATTTAAATGGGAAGGTCATGAACCTTTGAAGCGGTGGCGTC 300
QY 313 GTTACTGTAAACCAGGATTCAGTTTGACAGATGGCTGTTTCATCTACAGGTCAGTTTC 372
DB 301 GTTACTGTAAACCAGGATTCAGTTTGACAGATGGCTGTTTCATCTACAGGTCAGTTTC 360
QY 373 ATTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAGACATGGGCTGGAA 432
DB 361 ATTGGCGTGAACCTTCTCCGATGAGACCTGTTATGCAAAAGAGACATGGGCTGGAA 420
QY 433 GCCAGCACTGAGCGTTTGTATCTCTCGTATGCGGTGTGAAAAGAGATTCATAAGGCT 492
DB 421 GCCAGCACTGAGCGTTTGTATCTCTCGTATGCGGTGTGAAAAGAGATTCATAAGGCT 480
QY 493 CTGAAGCTGAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG 552
DB 481 CTGAAGCTGAAAGACGGGTGTCATTACCTAGTTGAATTCAAAAGTATTTACATGGCAAG 540
QY 553 AAGCCTGTGACGTAACCAAGGTACTACTATGTTGACTCCAAACTGATTAACAAGCCAC 612
DB 541 AAGCCTGTGACGTAACCAAGGTACTACTATGTTGACTCCAAACTGATTAACAAGCCAC 600
QY 613 AACGAAGCTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGCCACCATCTGTTTC 672
DB 601 AACGAAGCTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGCCACCATCTGTTTC 660
QY 673 CTTTA 677
DB 661 CTTTA 665
RESULT 11
AAD03615
ID AAD03615 standard; cDNA; 898 BP.
XX
AC AAD03615;
XX
DT 11-SEP-2003 (revised)
DT 19-JUN-2001 (first entry)
XX
DE Discosoma sp. red chromo/fluorescent protein, drFP583 (NFP-6) cDNA.
XX
KM Anthozoa; Chromoprotein; fluorescent protein; drFP583; NFP-6; sunscreen;
KM analyte detection assay; selectable marker; recombinant DNA application;
KM biosensor; pH indicator; invivo marker; selective filter; ss.
XX
OS Discosoma sp; red.
XX
FH Key Location/Qualifiers
FT CDS 93..770
FT /*tag= a
FT /product= "Chromo/fluorescent protein, drFP583 (NFP-6) "
FT /transl_except= (pos:540..600, aa:Leu-Gly)
FT /note= "Insertion of 60 bases alters the reading frame"
XX
PN WO200127150-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028477.
XX
PR 14-OCT-1999; 99US-00418529.
PR 15-OCT-1999; 99US-00418917.
PR 15-OCT-1999; 99US-00418922.
PR 19-NOV-1999; 99US-00444338.
PR 19-NOV-1999; 99US-00444341.
PR 09-DEC-1999; 99US-00457556.
PR 09-DEC-1999; 99US-00457898.
PR 09-DEC-1999; 99US-00458144.
PR 09-DEC-1999; 99US-00458477.

PR 10-DEC-1999; 99WO-US029405.
PR 14-JUN-2000; 2000US-0211607P.
PR 14-JUN-2000; 2000US-0211609P.
PR 14-JUN-2000; 2000US-0211626P.
PR 14-JUN-2000; 2000US-0211627P.
PR 14-JUN-2000; 2000US-0211687P.
PR 14-JUN-2000; 2000US-0211766P.
PR 14-JUN-2000; 2000US-0211880P.
PR 14-JUN-2000; 2000US-0211888P.
PR 14-JUN-2000; 2000US-0212070P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov SA, Fradkov AE, Labas YA, Matz MV, Tersikh A;
XX
DR WPI; 2001-266409/27.
DR P-PSDB; AAE00375.
XX
PT An Anthozoa chromo- or fluorescent protein (P1) present in an environment
PT other than its natural environment, useful as a label in analyte
PT detection assays and as a selectable marker in recombinant DNA
PT applications.
XX
PS Claim 13; Fig 6; 69pp; English.
XX
CC The present sequence is a Discosoma sp. red chromo/fluorescent protein,
CC drFP583 (NFP-6) cDNA. NFP-6 is present in an environment other than its
CC natural environment and has an absorbance maximum ranging from 250nm to
CC 750nm and more usually from 540nm to 580nm and emission maximum ranging
CC from 275nm to 775nm and more usually from 565 to 605nm. The
CC chromoproteins or fluorescent proteins are useful as labels in analyte
CC detection assays, as selectable markers in recombinant DNA applications,
CC as biosensors in prokaryotic and eukaryotic cells e.g. as pH indicator
CC and as in vivo markers in animals. They are also useful in sunscreens and
CC as selective filters. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 898 BP; 273 A; 173 C; 240 G; 212 T; 0 U; 0 Other;
Query Match 97.2%; Score 658.8; DB 4; Length 898;
Best Local Similarity 98.2%; Pred. No. 1.3e-201;
Matches 666; Conservative| 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAAAGATGTTATCAAGAGTTCATGAGGTTTAAAGCTTCGCATGAAGCA 60
DB 93 ATGAGGCTTCCAAAGATGTTATCAAGAGTTCATGAGGTTTAAAGCTTCGCATGAAGCA 152
QY 61 ACGGTCAATGGGCACGAGTTTGAATAAGAGCGAAGAGAGGGAGGCCATACGAAGGC 120
DB 153 ACGGTCAATGGGCACGAGTTTGAATAAGAGCGAAGAGAGGGAGGCCATACGAAGGC 212
QY 121 CACAATACCGTTAAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 180
DB 213 CACAATACCGTTAAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGT 272
QY 181 TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAGCAACCCTGCCACATACCA 240
DB 273 TTGTCACCACAATTTCAGTATGGAAGCAAGGTATATGTCAGCAACCCTGCCACATACCA 332
QY 241 GACTATTAATAAGCTGTTCATTTCTGGAAGGATTTAAATGGGAAAGGTCATGAACCTTGA 300
DB 333 GACTATTAATAAGCTGTTCATTTCTGGAAGGATTTAAATGGGAAAGGTCATGAACCTTGA 392
QY 301 GACGCTGCGTCTGTTACTGTAAACCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
DB 393 GACGCTGCGTCTGTTACTGTAAACCAGGATTCAGTTTGACAGATGGCTGTTTCATCTAC 452
QY 361 AAGTCAAGTTCAATTGGCGTGAACCTTCTCCGATGAGCCTGTATGCAAAAGAGACA 420
DB 453 AAGTCAAGTTCAATTGGCGTGAACCTTCTCCGATGAGCCTGTATGCAAAAGAGACA 512
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGTGTGAAGAGAGAG 480
DB 513 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGGCGTGTGAAGAGAGAG 572

QY 481 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAGTATT 540
|||||
Db 573 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAGTATT 632
QY 541 TACATGGCAAGAAGCGCTGTGACAGCTACCAGGGTACTACTATGTTGACTCCAACTGGAT 600
|||||
Db 633 TACATGGCAAGAAGCGCTGTGACAGCTACCAGGGTACTACTATGTTGACTCCAACTGGAT 692
QY 601 ATACAAGCCACAAGCAAGACTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGC 660
|||||
Db 693 ATACAAGCCACAAGCAAGACTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGC 752
QY 661 CACCATCTGTTCTTTAA 678
|||||
Db 753 CACCATCTGTTCTTTAA 770
RESULT 12
AAA48742
ID AAA48742 standard; cDNA; 898 BP.
XX
AC AAA48742;
XX
DT 15-SEP-2003 (revised)
DT 19-SEP-2000 (first entry)
XX
DE Discosoma sp. "red" novel fluorescent protein drFP583 cDNA.
XX
XX Anthozoa; drFP583; fluorescent protein; non-bioluminescent organism;
KM fluorescent labeling; ss.
XX
OS Discosoma sp; "red".
XX
FH Key location/Qualifiers
FT CDS 93..770
FT /product= "drFP583"
FT /transl_except= (pos:456..457,aa:Val)
FT /transl_except= (pos:470..473,aa:Val)
FT /note= "The codon at position 456..457 has an apparent 1
FT nucleotide deletion which alters the reading frame. The
FT codon at position 470..473 has an apparent 1 nucleotide
FT insertion which corrects the altered reading frame"
XX
PN WO200034326-A1.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029473.
XX
PR 11-DEC-1998; 98US-00210330.
PR 14-OCT-1999; 99US-00418529.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov SA, Fradkov AF, Labas YA, Matz MV, Green G, Chen Y;
PI Ding L;
XX
DR WPI; 2000-423381/36.
XX
PT Novel fluorescent protein from non-bioluminescent Discosoma sp. red,
PT useful for fluorescent labeling and as markers.
XX
PS Claim 6; Page 73-74; 86pp; English.
XX
CC The present sequence is the cDNA sequence of drFP583 from Discosoma sp.
CC "red", a non-bioluminescent species of the Class Anthozoa. drFP583 is a
CC full-length cDNA encoding a novel fluorescent protein (nFP). Fluorescent
CC proteins can be used in fluorescent labeling, a useful tool for marking a
CC protein, cell or organism of interest. Unlike other markers used in
CC protein labeling, such as beta-galactosidase and luciferase, fluorescent
CC proteins do not require an exogenous cofactor or substrate. Methods
CC involving fluorescent proteins are also less laborious and less difficult

CC to control than the traditional methods of fluorescent labeling, where a
CC protein of interest is purified and then covalently conjugated to a
CC fluorophore derivative. Novel fluorescent proteins isolated from species
CC of the Class Anthozoa can be used as markers for gene expression and
CC protein localization studies, and in fluorescence resonance energy
CC transfer (FRET) reactions. They may have improved properties and better
CC suitability for larger excitations compared to prior art fluorescent
CC proteins such as green fluorescent protein. (Updated on 15-SEP-2003 to
CC standardise OS field)
XX
SQ Sequence 898 BP; 273 A; 172 C; 240 G; 213 T; 0 U; 0 Other;
Query Match 96.9%; Score 657.2; DB 3; Length 898;
Best Local Similarity 98.1%; Pred. No. 4.3e-201;
Matches 665; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 1 ATGAGGCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAAGTTCCGATGAAGGA 60
|||||
Db 93 ATGAGGCTTCCAAGATGTTATCAAGAGTTTCATGAGGTTTAAAGTTCCGATGAAGGA 152
QY 61 ACGGTCATGGGCACGAGTTTGAATAGAAGCGGAGAGAGAGGGGACCATACGAAGGC 120
|||||
Db 153 ACGGTCATGGGCACGAGTTTGAATAGAAGCGGAGAGAGGGGACCATACGAAGGC 212
QY 121 CACAATACCGTAAAGCTTAAGGTACCAAGGGGGACCTTTGCCATTGCTGGGATATT 180
|||||
Db 213 CACAATACCGTAAAGCTTAAGGTACCAAGGGGGACCTTTGCCATTGCTGGGATATT 272
QY 181 TTGTACCAACAATTTAGTATGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 240
|||||
Db 273 TTGTACCAACAATTTAGTATGAAGCAAGGTATATGTCAAGCACCTGCGACATACCA 332
QY 241 GACTATAAAAGCTGTCTATTTCTGGAAGATTTAATGGGAAAGGTCATGAACTTGAA 300
|||||
Db 333 GACTATAAAAGCTGTCTATTTCTGGAAGATTTAATGGGAAAGGTCATGAACTTGAA 392
QY 301 GACGGTGGCGCTTAAGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 360
|||||
Db 393 GACGGTGGCGCTTAAGTAAACCCAGATTCAGTTTGACAGATGGCTGTTTCATCTAC 452
QY 361 AAGGTCAAGTTCATTGGCGTGAACCTTCCGATGAGACCTGTATGCAAAAGAAGACA 420
|||||
Db 453 AAGTCAAGTTCATTGGCGTGAACCTTCCGATGAGACCTGTATGCAAAAGAAGACA 512
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGCGGTGAAAGAGAG 480
|||||
Db 513 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGTATCCTCGTATGCGGTGAAAGAGAG 572
QY 481 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAGTATT 540
|||||
Db 573 ATTCATAAGGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAGTATT 632
QY 541 TACATGGCAAGAAGCGCTGTGACAGCTACCAGGGTACTACTATGTTGACTCCAACTGGAT 600
|||||
Db 633 TACATGGCAAGAAGCGCTGTGACAGCTACCAGGGTACTACTATGTTGACTCCAACTGGAT 692
QY 601 ATACAAGCCACAAGCAAGACTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGC 660
|||||
Db 693 ATACAAGCCACAAGCAAGACTATACATCGTTGAGCAGTATGAAGAACCAGGAGCGC 752
QY 661 CACCATCTGTTCTTTAA 678
|||||
Db 753 CACCATCTGTTCTTTAA 770
RESULT 13
AAA28958
ID AAA28958 standard; cDNA; 876 BP.
XX
AC AAA28958;
XX
DT 12-SEP-2000 (first entry)
XX

DE Discosoma sp. "magenta" dmFP592 cDNA encoding a fluorescent protein.
XX
KW dmFP592; fluorescent protein; non-bioluminescent; label; marker;
KM fluorescence resonance energy transfer reaction; FRET; ss.
XX
OS Discosoma sp.
XX
FH Key Location/Qualifiers
FT CDS 45..737
FT /+tag= a
FT /product= "fluorescent_protein"
XX
PN WO200034324-A1.
XX
PD 15-JUN-2000.
XX
PF 10-DEC-1999; 99WO-US029412.
XX
PR 11-DEC-1998; 98US-00210330.
PR 19-NOV-1999; 99US-00444341.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov SA, Fradkov AF, Labas YA, Maltz MV;
XX
DR WPI; 2000-423379/36.
DR P-PSDB; AAY92894.
XX
PT Novel fluorescent protein from non-bioluminescent Discosoma species,
PT useful for fluorescent labeling and as markers.
XX
PS Claim 7; Page 54-55; 60pp; English.
XX
CC This cDNA encodes a fluorescent protein (dmFP592) from Discosoma sp.
CC "magenta", a non-bioluminescent species of the genera Anthozoa. The
CC fluorescent colour is observed under usual white light or ultraviolet
CC light. It has an absorbance maximum at 573 nm and an emission maximum at
CC 593 nm. The polynucleotides of the invention can be used to produce the
CC proteins recombinantly, and as a source of primers and probes for
CC identifying related proteins. The fluorescent markers for gene expression
CC in fluorescent labeling, as fluorescent markers for gene expression and
CC protein localization studies, and in fluorescence resonance energy
CC transfer (FRET) reactions. They may have improved properties and better
CC suitability for larger excitations, compared to prior art fluorescent
CC proteins such as green fluorescent protein from Aequorea victoria, which
CC has an excitation maximum at 395 nm, a second excitation peak at 475 nm
CC and an emission maximum at 510 nm
XX
SQ Sequence 876 BP; 256 A; 165 C; 232 G; 223 T; 0 U; 0 Other;
Query Match 83.5%; Score 566.4; DB 3; Length 876;
Best Local Similarity 90.6%; Pred. No. 8.3e-172;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;
QY 1 ATGAGGCTTCCAGAATGTTATCAAGGAGTTGATGAGTTTAAAGTTGCGATGGAAGCA 60
DB 45 ATGAGTTGTTCCAAGAATGTGATCAAGGAGTTGATGAGTTCAAGGTTGCTATGGAAGGA 104
QY 61 ACGGTCAATGGGACGAGTTTGAATAGAGCGAAGAGAGAGGGGAGCCATACGAAGGC 120
DB 105 ACGGTCAATGGGACGAGTTTGAATAGAGCGAAGAGAGGGGAGCCCTTACGAAGGT 164
QY 121 CACAATACCGTAAGCTTAAGGTAACCAAGGGGAGACCTTTGCCATTGCTTGGATATT 180
DB 165 CACTGTTCCGTAAGCTTATGTAACCAAGGGTGACCTTTGCCATTGCTTTGATATT 224
QY 181 TTGTCAACCAATTTCAGTATGGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240
DB 225 TTGTCAACCAATTTCAGTATGGAAGCAAGGTATATGTCAAAACCCCTGCCACATACCA 284
QY 241 GACTATATAAAGCTGTCATTCTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTGA 300
DB 285 GACTATATAAAGCTGTCATTCTCTGAAGGATTTAAATGGGAAAGGGTCATGAACCTTGA 344

QY 301 GACGTGGCGTCTGTTACTGTAACCCAGATTCCAGTTTGCAAGATGGCTGTTTCATCTAC 360
DB 345 GACGTGGCGTGTGTTACTGTAATCCCAAGATTCAGTTTGAAAAGCGGCTGTTTCATCTAC 404
QY 361 AAGTCAAGTTCATTGGCGGTGAACCTTCCGATGGAACCTGTTATGCAAAAAGAGACA 420
DB 405 GAGGTCAAGTTCATTGGGGTGAACCTTCCGATGGAACCTGTTATGCAAGAGAGACA 464
QY 421 ATGGGCTGGGAAGCCAGCACTGAGCGTTTGATCCTCGTATGGCGGTGTTGAAGAGAG 480
DB 465 CGGGGCTGGGAAGCCAGCTCTGAGCGTTTGATCCTCGTATGGGGTCTGAAGAGAGAC 524
QY 481 ATTCATTAAGGCTCTGAAGCTGAAGAAGCGGTGTCATTACCTAGTTGAATTCAAAAGTATT 540
DB 525 ATCCATATGGCTCTGAGGCTGGAAGAGGCGGCCATTACCTCGTTGAATTCAAAAGTATT 584
QY 541 TACATGGCAAGAAGCCT--GTGCAGCTACGAGGTACTACTATGTTGACTCCAAACTG 597
DB 585 TACATGGTAAAGAAGCCTTCAGTGCAGTTGCCAGGCTACTATTATGTTGACTCCAAACTG 644
QY 598 GATATTAACAAGCCACAAGCAAGACTATACATCGTTGAGCAAGTATGAAGAACCAGGGA 657
DB 645 GATATGACGAGCCACAAGCAAGATTACACAGTCGTTGAGCAAGTATGAAAAAACCAGGGA 704
QY 658 CGCCACCATCTGTTCCCTTA 677
DB 705 CGCCACCATCCGTTCAATTAA 724
RESULT 14
AAD03618
ID AAD03618 standard; cDNA; 876 BP.
XX
AC AAD03618;
XX
DT 11-SEP-2003 (revised)
DT 19-JUN-2001 (first entry)
XX
DE Discosoma sp. magenta chromo/fluorescent protein, dmFP592 (NFP-9) cDNA.
XX
KW Anthozoa; Chromoprotein; fluorescent protein; dmFP592; NFP-9; sunscreen;
KW analyte detection assay; selectable marker; recombinant DNA application;
KW biosensor; pH indicator; invivo marker; selective filter; ss.
XX
OS Discosoma sp; magenta.
XX
FH Key Location/Qualifiers
FT CDS 45..737
FT /+tag= a
FT /product= "Chromo/fluorescent protein, dmFP592 (NFP-9) "
XX
PN WO200127150-A2.
XX
PD 19-APR-2001.
XX
PF 13-OCT-2000; 2000WO-US028477.
XX
PR 14-OCT-1999; 99US-00418529.
PR 15-OCT-1999; 99US-00418917.
PR 15-OCT-1999; 99US-00418922.
PR 19-NOV-1999; 99US-00444338.
PR 19-NOV-1999; 99US-00444341.
PR 09-DEC-1999; 99US-00457556.
PR 09-DEC-1999; 99US-00457898.
PR 09-DEC-1999; 99US-00458144.
PR 09-DEC-1999; 99US-00458477.
PR 10-DEC-1999; 99WO-US029405.
PR 14-JUN-2000; 2000US-0211607P.
PR 14-JUN-2000; 2000US-0211609P.
PR 14-JUN-2000; 2000US-0211626P.
PR 14-JUN-2000; 2000US-0211627P.
PR 14-JUN-2000; 2000US-0211687P.

PR 14-JUN-2000; 2000US-0211766P.
PR 14-JUN-2000; 2000US-0211880P.
PR 14-JUN-2000; 2000US-0211888P.
PR 14-JUN-2000; 2000US-0212070P.
XX
PA (CLON-) CLONTECH LAB INC.
XX
PI Lukyanov SA, Fradkov AF, Labas YA, Matz MV, Tersikh A;
XX
DR WPI; 2001-266409/27.
DR P-PSDB; AAE00378.
XX
PT An Anthozoa chromo- or fluorescent protein (P1) present in an environment
PT other than its natural environment, useful as a label in analyte
PT detection assays and as a selectable marker in recombinant DNA
PT applications.
XX
PS Claim 13; Fig 9; 69pp; English.
XX
CC The present sequence is a Discosoma sp. magenta chromo/fluorescent
CC protein, dmFP592 (NFP-9) cDNA. NFP-9 is present in an environment other
CC than its natural environment and has an absorbance maximum ranging from
CC 375nm to 775nm and more usually from 560nm to 590nm and emission maximum
CC ranging from 395nm to 795nm and more usually from 580 to 610nm. The
CC chromoproteins or fluorescent proteins are useful as labels in analyte
CC detection assays, as selectable markers in recombinant DNA applications,
CC as biosensors in prokaryotic and eukaryotic cells e.g. as pH indicator
CC and as in vivo markers in animals. They are also useful in sunscreens and
CC as selective filters. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 876 BP; 256 A; 165 C; 232 G; 223 T; 0 U; 0 Other;

Query Match 83.5%; Score 566.4; DB 4; Length 876;
Best Local Similarity 90.6%; Pred. No. 8.3e-172;
Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

QY 1 ATGAGGTCTTCCAAGAATGTTATCAAGAGTTCATGAGTTTAAGTTCGCATGAAGGA 60
DB 45 ATGAGTTGTTCCAAGAATGTGATCAAGAGTTCATGAGTTCAAGTTCGATGAAGGA 104

QY 61 ACGGTCAATGGGACACGAGTTTGAATAGAAAGCCGAAGAGAGGGGCCATACGAAGGC 120
DB 105 ACGGTCAATGGGACGAGTTTGAATAAAGCCGAAGGTGAAGGGCCCTTACGAAGGT 164

QY 121 CACAATACCGTAAAGCTTAAAGGTAACCAAGGGGGGACCTTTGCCATTGCTTGGGATATT 180
DB 165 CACTGTTCGGTAAAGCTTATGATAACCAAGGGGTGACCTTTGCCATTGCTTTTGATATT 224

QY 181 TTGTCAACCAATTCAGTATGAAGCAAGGTATATGTCAAGCACCCCTGCCACATACCA 240
DB 225 TTGTCAACCAATTCAGTATGAAGCAAGGTATATGTCAAAACACCCTGCCACATACCA 284

QY 241 GACTATAAAAAAGCTGTCACTTCTCGAAGATTTAAATGGAAAGGTCATGAACCTTTGAA 300
DB 285 GACTATAAAAAAGCTGTCACTTCTCGAGGATTTAAATGGAAAGGTCATGAACCTTTGAA 344

QY 301 GACGGTGGCGTCTACTGTAAACCCAGGATTCAGTTTGACAGATGCGTGTTCATCTAC 360
DB 345 GACGGTGGCGTGTACTGTATCCCAAGATTCAGTTTGAAGAAGCGGCTGTTTCATCTAC 404

QY 361 AAGGTCAAGTTCATTTGGGTTGAACCTTCTCCGATGGAACCTGTTATGCAAAAGAGACA 420
DB 405 GAGGTCAAGTTCATTTGGGTTGAACCTTCTCTGATGACCTGTTATGCAAGAGAGACA 464

QY 421 ATGGCTGGGAAGCCAGACATGAGCGTTTGTATCCTCGTATGGCGGTGTGAAGAGAGAG 480
DB 465 CGGGGCTGGGAAGCCAGCTCTGAGCGTTTGTATCCTCGTATGGGCTGTGAAGAGAGAC 524

QY 481 ATTCAATAGGCTCTGAGCTGAAGAGAGCGGTGTCACTTACCTAGTTGAATCAAAAGTATT 540
DB 525 ATCCATATGCTCTGAGGCTGAAGAGAGGCGGCATTAACCTCGTTGAATCAAAAGTATT 584

QY 541 TACATGGCAAGAAGCCT---GTGAGCTACCAAGGTACTATATGTTGACTCCAAACTG 597

DB 585 TACATGTTAAAGAGCCCTTCAGTGCAGTTGCCAGGCTACTATATATGTTGACTCCAAACTG 644
QY 598 GATATAACAAGCCACAAACGAAGACTATACAATCGTTGAGCAGTATGAAGAACCAGAGGA 657
DB 645 GATATGACGAGCCACAAACGAAGATTACACAGTCGTTGAGCAGTATGAAAAAAACCCAGGGA 704
QY 658 CGCCACCATCTGTTCTTTA 677
DB 705 CGCCACCATCCGTTCAATTAA 724

RESULT 15
ACC44649
ID ACC44649 standard; DNA; 876 BP.
XX
AC ACC44649;
XX
DT 29-MAY-2003 (first entry)
XX
DE Red fluorescent protein (DsRed) encoding DNA SEQ ID NO:39.
XX
KW Chromosome-based platform; artificial chromosome; eukaryotic chromosome;
KW att site; integrase; recombinase; Aces; gene therapy; transgenic animal;
KW platform artificial chromosome expression system; gene; ds.
XX
OS Discosoma sp.
OS Synthetic.
XX
PN WO200297059-A2.
XX
PD 05-DEC-2002.
XX
PF 30-MAY-2002; 2002WO-US017452.
XX
PR 30-MAY-2001; 2001US-0294758P.
PR 21-MAR-2002; 2002US-0366891P.
XX
PA (CHRO-) CHROMOS MOLECULAR SYSTEMS INC.
XX
PI Perkins E, Perez C, Lindenbaum M, Greene A, Leung J, Fleming E;
PI Stewart S, Shellard J;
XX
DR WPI; 2003-140461/13.
DR P-PSDB; ABP96651.
XX
PT Novel eukaryotic chromosome comprising one or many att sites which
PT permits site-directed integration in the presence of lambda-integrase,
PT useful for site-specific recombination-directed integration of DNA of
PT interest.
XX
PS Example 1; Page 191-192; 272pp; English.
XX
CC The present invention describes a eukaryotic chromosome (I) comprising
CC one or several att sites, where an att site is heterologous to the
CC chromosome, and permits site-directed integration in the presence of
CC lambda-integrase. Also described: (1) a platform artificial chromosome
CC expression system (Aces) (II) comprising several sites that participate
CC in recombinase catalysed recombination; and (2) a method (M1) for
CC introducing a heterologous nucleic acid into a platform artificial
CC chromosome. (I) can be used in gene therapy. (M1) is useful for
CC introducing a heterologous nucleic acid molecule into a platform
CC artificial chromosome, preferably an Aces. (II) is useful for producing a
CC transgenic animal (e.g. a fish, insect, reptile, amphibian, arachnid, or
CC mammal) by introducing (II) by cell fusion, lipid-mediated transfection,
CC by a carrier system, microinjection, microcell fusion, electroporation,
CC microprojectile bombardment or direct DNA transfer into an embryonic
CC cell, preferably a stem cell or an embryo. (II) comprises a heterologous
CC nucleic acid that encodes a therapeutic product which is useful for
CC making a library of Aces comprising random portions of a genome. ACC44612
CC to ACC44732 and ABP96650 to ABP96657 represent sequences used in the
CC exemplification of the present invention
XX

SQ Sequence 876 BP; 256 A; 165 C; 232 G; 223 T; 0 U; 0 Other;

Query Match 83.5%; Score 566.4; DB 7; Length 876;

Best Local Similarity 90.6%; Pred. No. 8.3e-172;

Matches 616; Conservative 0; Mismatches 61; Indels 3; Gaps 1;

```
QY      1 ATGAGGTCTTCCAAGAATGTATATCAGAGGTTTCATGAGTTTAAGTTTCGATGGAAGG 60
      |||||
DB      45 ATGAGTTGTTCCAAGATGTGATCAAGAGTTTCATGAGTTCAAGGTTTCTATGGAAGG 104

QY      61 ACCGTCAATGGGCGACGAGTTTGAATATGAAGCGGAAGAGAGAGGGCCATACGAAGGC 120
      |||||
DB      105 ACCGTCAATGGGCGACGAGTTTGAATATGAAGCGGAAGAGAGAGGGCCATACGAAGGT 164

QY      121 CACAATACCGTAAAGCTTAAGTTAACCAAGGGGGACCTTTGCCATTGCTTGGATATT 180
      |||||
DB      165 CACTGTTCCGTAAGCTTATAGTTAACCAAGGGTGACCTTTGCCATTGCTTTGATATT 224

QY      181 TTGTACACCAATTTCAGTATGAAGCAAGGTATATGTCAAGCACCTGCCGACATACCA 240
      |||||
DB      225 TTGTACACCAATTTCAGTATGAAGCAAGGTATATGTCAAAACACCTGCCGACATACCA 284

QY      241 GACTATAAAAAGCTGTCTATTCTCGAAGATTAAATGGGAAAGGTCATGAACCTTGAA 300
      |||||
DB      285 GACTATAAAAAGCTGTCTATTCTCGAAGATTAAATGGGAAAGGTCATGAACCTTGAA 344

QY      301 GACGGTGGCGCTTACTGTAAACCCAGATTCCAGTTTGACAGATGGCTGTTTCATCTAC 360
      |||||
DB      345 GACGGTGGCGCTTACTGTATCCCAAGATTCCAAGTTGAAAGACGGCTGTTTCATCTAC 404

QY      361 AAGGTCAAGTTCATTGGCGTGAACCTTCTCCGATGAGCCTGTTATGCAAAAAGAGACA 420
      |||||
DB      405 GAGGTCAAGTTCATTGGGGTGAACCTTCTCTGATGAGCCTGTTATGACAGAGAGACA 464

QY      421 ATGGGCTGGGAAGCCAGCACTGAGCGTTGTATCCTCGTATGGCGGTGAAAGGAGAG 480
      |||||
DB      465 CGGGGCTGGGAAGCCAGCTCTGAGCGTTGTATCCTCGTATGGGGTCTGAAGAGAGAC 524

QY      481 ATTCAATAAGCTCTGAAGCTGAAAGACGGTGTCTATTACCTAGTTGAATTCAAAAGTATT 540
      |||||
DB      525 ATCCATATGGCTCTGAGGCTGGAAGAGGGCCCATTAACCTCGTTGAATTCAAAAGTATT 584

QY      541 TACATGGCAAAAGAGCCT--GTGCACTAACCAAGGGTACTACTATGTGACTCCAAACTG 597
      |||||
DB      585 TACATGGTAAAGAGCCTTCACTGCAAGCTCAAGGCTACTATATGTGACTCCAAACTG 644

QY      598 GATATAACAGCCACAACGAAGACTATTAATCGTTGAGCAGTATGAAGAAGCGAGGGA 657
      |||||
DB      645 GATATGACGAGCCACAACGAAGATTAACAAGTGTGAGCAGTATGAAAAAAACCAGGGA 704

QY      658 CGCCACCATCTGTTCTTTA 677
      |||||
DB      705 CGCCACCATCCGTTCAATTAA 724
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Job time : 309 secs

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